



## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

<b>(51) International Patent Classification <sup>6</sup> :</b> <b>C12N 15/29, 15/82, C07K 14/415, 14/81,</b> <b>A01H 5/00, A23K 1/00, A23L 1/29, 1/305</b>	<b>A2</b>	<b>(11) International Publication Number:</b> <b>WO 98/20133</b> <b>(43) International Publication Date:</b> 14 May 1998 (14.05.98)
<b>(21) International Application Number:</b> PCT/US97/20441 <b>(22) International Filing Date:</b> 31 October 1997 (31.10.97) <b>(30) Priority Data:</b> 08/740,682 1 November 1996 (01.11.96) US <b>(71) Applicant (for all designated States except US):</b> PIONEER HI-BRED INTERNATIONAL, INC. [US/US]; Dar- win Building, 7100 N.W. 62nd Avenue, Johnston, IA 50131-1000 (US). <b>(72) Inventors; and</b> <b>(75) Inventors/Applicants (for US only):</b> RAO, Aragula, Gururaj [US/US]; 4734 74th Street, Urbandale, IA 50322-1158 (US). ROESLER, Keith, R. [US/US]; 3928 Patricia Drive, Urbandale, IA 50322 (US). <b>(74) Agents:</b> MICHEL, Marianne, H. et al.; Darwin Building, 7100 N.W. 62nd Avenue, Johnston, IA 50131-1000 (US).	<b>(81) Designated States:</b> AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).  <b>Published</b> <i>Without international search report and to be republished upon receipt of that report.</i>	
<b>(54) Title:</b> PROTEINS WITH ENHANCED LEVELS OF ESSENTIAL AMINO ACIDS  <b>(57) Abstract</b>  The present invention provides for polypeptides comprising protease inhibitors with increased amounts of essential amino acids and nucleotides encoding for these peptides. Also provided are transformed plants and seeds with enhanced nutritional value due to the expression of modified polypeptides.		

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**PROTEINS WITH ENHANCED LEVELS  
OF ESSENTIAL AMINO ACIDS**

**Field of the Invention**

5       The present invention relates to the field of protein engineering wherein changing amino acid compositions effects improvements in the nutrition content of feed. Specifically, the present invention relates to methods of enhancing the nutritional content of animal feed by expressing derivatives of a protease inhibitor to provide higher percentages of essential amino acids in plants.

**Background of the Invention**

10       Feed formulations are required to provide animals essential nutrients critical to growth. However, crop plants are generally rendered food sources of poor nutritional quality because they contain low proportions of several amino acids which are essential  
15       for, but cannot be synthesized by, monogastric animals.

For many years researchers have attempted to improve the balance of essential amino acids in the seed proteins of important crops through breeding programs. As more becomes known about seed storage proteins and the expression of the genes which encode these proteins, and as transformation systems are developed for a greater variety of plants,  
20       molecular approaches for improving the nutritional quality of seed proteins can provide alternatives to the more conventional approaches. Thus, specific amino acid levels can be enhanced in a given crop via biotechnology.

One alternative method is to express a heterologous protein of favorable amino acid composition at levels sufficient to obviate feed supplementation. For example, a  
25       number of seed proteins rich in sulfur amino acids have been identified. A key to good expression of such proteins involves efficient expression cassettes with tissue-preferred promoters. Not only must the gene-controlling regions direct the synthesis of high levels of mRNA, the mRNA must be translated into a stable protein and over expression of this protein must not be detrimental to plant or animal health.

30       Among the essential amino acids needed for animal nutrition, often limiting in crop plants, are methionine, threonine, lysine, isoleucine, leucine, valine, tryptophan, phenylalanine, and histidine. Attempts to increase the levels of these free amino acids by

breeding, mutant selection and/or changing the composition of the storage proteins accumulated in crop plants has met with limited success.

A transgenic example is the phaseolin-promoted Brazil nut 2S expression cassette. However, even though Brazil nut protein increases the amount of total methionine and bound methionine, thereby improving nutritional value, there appears to be a threshold limitation as to the total amount of methionine that is accumulated in the seeds. The seeds remain insufficient as sources of methionine and methionine supplementation is required in diets utilizing the above soybeans.

An alternative to the enhancement of specific amino acid levels by altering the levels of proteins containing the desired amino acid is modification of amino acid biosynthesis. Recombinant DNA and gene transfer technologies have been applied to alter enzyme activity catalyzing key steps in the amino acid biosynthetic pathway. See Glassman, U.S. Patent No. 5,258,300; Galili, et al., European Patent Application No. 485970; (1992); incorporated herein in its entirety. However, modification of the amino acid levels in seeds is not always correlated with changes in the level of proteins that incorporate those amino acids. See Burrow, et al., Mol. Gen. Genet.; Vol. 241; pp. 431-439; (1993); incorporated herein in its entirety by reference. Increases in free lysine levels in leaves and seeds have been obtained by selection for DHDPS mutants or by expressing the E. coli DHDPS in plants. However, since the level of free amino acids in seeds, in general, is only a minor fraction of the total amino acid content, these increases have been insufficient to significantly increase the total amino acid content of seed.

The lysC gene is a mutant bacterial aspartate kinase which is desensitized to feedback inhibition by lysine and threonine. Expression of this gene results in an increase in the level of lysine and threonine biosynthesis. However, expression of this gene with seed-specific expression cassettes has resulted in only a 6-7% increase in the level of total threonine or lysine in the seed. See Karchi, et al., The Plant J.; Vol. 3; pp. 721-7; (1993); incorporated herein in its entirety by reference. Thus, there is minimal impact on the nutritional value of seeds, and supplementation with essential amino acids is still required.

In another study (Falco et al., *Biotechnology* 13:577-582, 1995), manipulation of bacterial DHDPs and aspartate kinase did result in useful increases in free lysine and total

seed lysine. However, abnormal accumulation of lysine catabolites was also observed suggesting that the free lysine pool was subject to catabolism.

Based on the foregoing, there exists a need for methods of increasing the levels of essential amino acids in seeds of plants. As can be seen from the prior art, previous approaches have led to insufficient increases in the levels of both free and bound amino acids and insignificant enhancement of the nutritional content of the feed.

### **Summary of the Invention**

It is one object of the present invention to provide nucleic acids encoding protease inhibitors with modified levels of essential amino acids and antigenic polypeptide fragments thereof. It is an object to reduce the protease inhibitory activity in addition to modifying levels of essential amino acids and antigenic polypeptide fragments thereof. It is a further object of the present invention to provide transgenic plants comprising protease inhibitors with modified levels of essential amino acids. Additionally, it is an object of the present invention to provide methods for increasing the nutritional value of a plant and for providing an animal feed composition comprising the transgenic plants comprising protease inhibitors with modified levels of essential amino acids and reduced protease inhibitory activity. The protease inhibitor CI-2 has been modified to produce an 83 amino acid polypeptide and an amino-terminal truncated version of 65 amino acids residues.

Therefore, in one aspect, the present invention relates to a polypeptide comprising at least 10 contiguous amino acid residues from a protein having Seq. ID No. 2, 4, 6, 8, 10 or 12, 16, 18, 20, 22, 24 wherein the polypeptide, when presented to an interacting molecule, specifically binds to the molecule; wherein the interacting molecule is also capable of binding to the protein; wherein the polypeptide does not bind to the interacting molecule, which has been fully absorbed with the protein; and wherein the polypeptide exhibits reduced protease inhibitor activity compared to a wild-type protein. In one embodiment, the present invention relates to the above mentioned polypeptide comprising Seq. ID No. 2, 4, 6, 8, 10 or 12, 16, 18, 20, 22, 24 and the polypeptide wherein more than about 55%, but less than about 95%, more than about 55%, but less than about 90%, or more than about 55% but less than about 85%, of the amino acid residues are essential amino acids. In some embodiments, the essential amino acid is lysine, tryptophan, methionine, threonine or mixtures thereof. In some embodiments, the present invention relates to the

nucleic acid encoding the polypeptide referred to *supra* and in one embodiment, relates to the nucleic acid as DNA and in another embodiment to a second nucleic acid which is complementary to the DNA. Another embodiment relates to the polypeptide wherein more than about 10% but less than about 40% of the amino acid residues are essential amino acids. Another embodiment relates to the transformed plant containing the polypeptide *supra*. In some embodiments an animal feed composition is provided.

In another embodiment, the polypeptide referred to *supra*, comprises at least 20 contiguous amino acid residues. In one aspect, the present invention relates to this polypeptide which contains or is modified to contain essential amino acids at positions 1, 8, 11, 17, 19, 34, 41, 56, 59, 62, 65, 67 or 73. In another aspect, the present invention relates to polypeptide which contains or is modified to contain essential amino acids at positions 1,16,23,41,44,49 and 55. In other embodiments, the polypeptide comprises at least 30 contiguous amino acid residues.

In a further aspect, the present invention relates to the modification of amino acid residues in the active site of protease inhibitors. The above mentioned polypeptide contains, or is modified to contain, non-wild type amino acid residues at positions from about 53 to about 70. In some embodiments, the non-wild type amino acid residues are located at positions 58-60, 62, 65, or 67. In another embodiment, the polypeptide the non-wild type amino acid residue is located at position 59. In some embodiments, the present invention relates to the nucleic acid encoding the polypeptide referred to *supra*.

In yet another aspect, the present invention relates to the above mentioned polypeptide comprising at least 10 contiguous amino acid residues from a protein having Seq. ID No. 2, 4, 6, 8, 10 or 12, 16,18,20,22,24 wherein the interactive molecule is an antibody elicited when the polypeptide is presented as an immunogen. In another aspect the polypeptide is about 7.3 Kda or about 9.2 Kda and further comprises one or more additional amino terminal amino acid residues, and in some embodiments, the amino-terminal amino acid residue is methionine. In another embodiment, the polypeptide is a cleavage product and in yet another, the polypeptide is recombinantly produced.

In a further aspect, the present invention relates to an expression cassette comprising the nucleic acids as described *supra*, operably linked to a promoter providing

for protein expression. In some embodiments, the promoter provides for protein expression in plants and in others the promoter provides for protein expression in bacteria, yeast or virus.

5 In yet another aspect, the present invention is directed to transformed plant cells containing the expression cassette described *supra*.

In another aspect, the present invention is directed to transformed plants containing at least one copy of the expression cassette described *supra*. In some embodiments, there is a seed of this transformed plant.

10 Another aspect of this invention provides a polypeptide produced by substituting an essential amino acid for at least one but less than 50 amino acid residues in a protease inhibitor for enhancing nutritional value of feed.

In another aspect, the present invention relates to polypeptides *supra* wherein hydrogen bonding is disrupted in the active site loop of the inhibitor.

15 In yet another aspect, the present invention relates to the polypeptide *supra* which exhibits decreased protease inhibitor activity as compared to the wild-type protein which does not have substituted amino acid residues. In some embodiments nucleic acid encodes a protease inhibitor protein with decreased inhibitory activity.

20 In another aspect, the present invention relates to the polypeptide *supra* which exhibits less than about 30% of the inhibitor activity compared to corresponding wild-type protein which does not have substituted amino acid residues.

In another aspect, the present invention relates to a nucleic acid comprising the sequence of SEQ ID No. 1,3,5,7,9,11,15,17,19,21, or 23 or a nucleic acid having at least 70% identity thereto, wherein the nucleic acid encodes for a polypeptide which exhibits reduced protease inhibitor activity compared to a wild-type protein. In one embodiment, 25 the polypeptide exhibits 80% identity and in another embodiment, 90%.

In yet another aspect, the present invention relates to a nucleic acid encoding a protease inhibitor protein wherein nucleotides have been substituted to increase the number of essential amino acids in the encoded protein. In one embodiment, the inhibitor

protein is derived from a plant. In another embodiment, the inhibitor protein is a chymotrypsin inhibitor- like protein.

In another aspect, the present invention relates to an expression cassette comprising the nucleic acid encoding the polypeptide *supra*, operably linked to a promoter providing for protein expression. In some embodiments, the promoter provides for protein expression in plants. In some embodiments, the promoter provides for protein expression in bacteria, yeast or virus.

In yet another aspect, the transformed plant containing at least one copy of the expression cassette *supra*. In some embodiments, the transformed plant is a monocotyledonous plant and could be selected from the group consisting of maize, sorghum, wheat, rice and barley. In some embodiments, the transformed plant is a dicotyledonous plant and could be selected from the group consisting of soybean, alfalfa, canola, sunflower, tobacco, tomato and canola. Preferably, the transformed plant is maize or soybeans. In some embodiments seed is produced by the transformed plant. In some embodiments an animal feed composition is provided, and in some, the animal feed composition is the seed.

In another aspect, the present invention relates to transformed plant cells containing the expression cassette *supra*.

In another aspect, the present invention relates to a method for increasing the nutritional value of a plant comprising introducing into the cells of the plant the expression cassette *supra* to yield transformed plant cells and regenerating a transformed plant from the transformed plant cells.

The present invention provides a method for genetically modifying protease inhibitors to increase the level of at least, but not limited to one, essential amino acid in a plant so as to enhance the nutritional value of the plant. The methods comprise the introduction of an expression cassette into regenerable plant cells to yield transformed plant cells. The expression cassette comprises a nucleotide encoding a protease inhibitor operably linked to a promoter functional in plant cells.



A fertile transgenic plant is regenerated from the transformed cells, and seeds are isolated from the plant. The seeds comprise the polypeptide which is encoded by the DNA segment and which is produced in an amount sufficient to increase the amount of the essential amino acid in the seeds of the transformed plants, relative to the amount of the essential amino acid in the seeds of a corresponding untransformed plant, e.g., the seeds of a regenerated control plant that is not transformed or corresponding untransformed seeds isolated from the transformed plant.

Preferably, the substantiated amino acid is an essential amino acid. More preferably, tryptophan, threonine, methionine and lysine are the substituted essential amino acid. Even more preferably, the additional essential amino acid is lysine.

A preferred embodiment of the present invention is the introduction of an expression cassette into regenerable plant cells. Also preferred is the introduction of an expression cassette comprising a DNA segment encoding an endogenous or modified polypeptide sequence.

The present invention also encompasses variations in the sequences described above, wherein such variations are due to site-directed mutagenesis, or other mechanisms known in the art, to increase or decrease levels of selected amino acids of interest. For example, site-directed mutagenesis to increase levels of essential amino acids is a preferred embodiment.

The present invention also provides a fertile transgenic plant. The fertile transgenic plant contains an isolated DNA segment comprising a promoter and encoding a protein comprising a protease inhibitor, modified by increasing the number of essential amino acids, under the control of the promoter. The protease inhibitor is expressed as so that the level of essential amino acids in the seeds of the transgenic plant is increased above the level in the seeds of a plant which only differ from the seeds of the transgenic plant in that the DNA segment or the encoded seed protein is under the control of a different promoter. The DNA segment is transmitted through a complete normal sexual cycle of the transgenic plant to the next generation. The present invention provides nucleotide sequences encoding proteins containing higher levels of essential amino acids by the substitution of one or more of the amino acid residues in the protease inhibitor. Substitutions at one or more of, but not limited to, positions 1,8,11,17,19,34,41,56,59,62,67 and 73 of the wild type protein are substituted with

essential amino acids. The present invention also involves the expression of the present chymotrypsin inhibitor derivatives or any derived protease inhibitor in plants to provide higher percentages of essential amino acids in plants than wild type plants.

5 In a preferred embodiment of the present invention, the present derivatives also exhibit reduced protease inhibitor activity. This is achieved by substituting the amino acid residues from about amino acid residue 53 to about amino acid residue 70 with residues other than the wild type residues.

Methods for expressing the modified protease inhibitors and for using plants are also provided to enhance the nutritional value of animal feed.

10 It is therefore an object of the present invention to provide methods for increasing the levels of the essential amino acids in the seeds of plants used for animal feed.

It is a further object of the present invention to provide seeds for food and/or feed with higher levels of the essential amino acid, lysine, than wild type species of the same seeds.

15 It is a further object of the present invention to provide seeds for food and/or feed such that the level of the essential amino acids is increased such that the need for feed supplementation is greatly reduced or obviated.

It is one object of the present invention to provide nucleic acids encoding enzymes involved in protease inhibition and antigenic polypeptide fragments thereof. It is also an  
20 object of the present invention to provide protease inhibitor polypeptides and antigenic fragments thereof. It is a further object of the present invention to provide transgenic plants comprising protease inhibitor nucleic acids. Additionally, it is an object of the present invention to provide methods for modulating, in a transgenic plant, the expression of protease inhibitor polynucleotides of the present invention.

25 Therefore, in one aspect, the present invention relates to an isolated nucleic acid comprising a member selected from the group consisting of (a) a polynucleotide having at least 70% identity to a polynucleotide encoding a polypeptide selected from the group consisting of SEQ ID NOS: 2,4,6,8,10 and 12,16,18,20,22,24 wherein the polypeptide when presented as an immunogen elicits the production of an antibody which is  
30 specifically reactive to the polypeptide; (b) a polynucleotide which is complementary to the polynucleotide of (a); and (c) a polynucleotide comprising at least 30 contiguous nucleotides from a polynucleotide of (a) or (b). In some embodiments, the polynucleotide

has a sequence selected from the group consisting of SEQ ID NOS: 1,3,5,7,9 and 11, 15,17,19,21, or 23 . The isolated nucleic acid can be DNA.

In another aspect, the present invention relates to recombinant expression cassettes, comprising a nucleic acid as described, *supra*, operably linked to a promoter.

5 In some embodiments, the nucleic acid is operably linked in antisense orientation to the promoter.

In another aspect, the present invention is directed to a host cell transfected with the recombinant expression cassette as described, *supra*. In some embodiments, the host cell is a maize, rye, barley, wheat, sorghum, oats, millet, rice, triticale, sunflower, alfalfa, rapeseed or soybean cell.

10 In a further aspect, the present invention relates to an isolated protein comprising a polypeptide of at least 10 contiguous amino acids encoded by the isolated nucleic acid referred to, *supra*. In some embodiments, the polypeptide has a sequence selected from the group consisting of SEQ ID NOS: 2,4,6,8,10 and 12,16,18,20,22,24.

15 In another aspect, the present invention relates to an isolated nucleic acid comprising a polynucleotide of at least 30 nucleotides in length which selectively hybridizes under stringent conditions to a nucleic acid selected from the group consisting of SEQ ID NOS: 1,3,5,7,9 and 11, 15,17,19,21, 23 or a complement thereof. In some embodiments, the isolated nucleic acid is operably linked to a promoter.

20 In yet another aspect, the present invention relates to an isolated nucleic acid comprising a polynucleotide, the polynucleotide having at least 60% sequence identity to an identical length of a nucleic acid selected from the group consisting of SEQ ID NOS: 1,3,5,7,9 and 11, 15,17,19,21, 23 or a complement thereof.

In another aspect, the present invention relates to an isolated nucleic acid  
25 comprising a polynucleotide having a sequence of a nucleic acid amplified from a *Zea mays* nucleic acid library using the primers selected from the group consisting of: SEQ ID NOS: 25 and 26 or complements thereof. In some embodiments, the nucleic acid library is a cDNA library.

In another aspect, the present invention relates to a recombinant expression  
30 cassette comprising a nucleic acid amplified from a library as referred to *supra*, wherein the nucleic acid is operably linked to a promoter. In some embodiments, the present invention relates to a host cell transfected with this recombinant expression cassette In

some embodiments, the present invention relates to a protease inhibitor protein produced from this host cell.

In an additional aspect, the present invention is directed to an isolated nucleic acid comprising a polynucleotide encoding a polypeptide wherein: (a) the polypeptide  
5 comprises at least 10 contiguous amino acid residues from a first polypeptide selected from the group consisting of SEQ ID NOS: 2,4,6,8,10 and 12, 16,18,20,22,24 wherein said polypeptide, when presented as an immunogen, elicits the production of an antibody which specifically binds to said first polypeptide; (b) the polypeptide does not bind to antisera raised against the first polypeptide which has been fully immunosorbed with the  
10 first polypeptide; (c) the polypeptide has a molecular weight in non-glycosylated form within 10% of the first polypeptide.

In a further aspect, the present invention relates to a heterologous promoter operably linked to a non-isolated protease inhibitor polynucleotide encoding a polypeptide, wherein the polypeptide is encoded by a nucleic acid amplified from a  
15 nucleic acid library as referred to, *supra*.

In yet another aspect, the present invention relates to a transgenic plant comprising a recombinant expression cassette comprising a plant promoter operably linked to any of the isolated nucleic acids referred to *supra*. In some embodiments, the transgenic plant is *Zea mays*. The present invention also provides transgenic seed from the transgenic plant.

20 In a further aspect, the present invention relates to a method of providing a modified protease inhibitor in a plant, comprising the steps of (a) transforming a plant cell with a recombinant expression cassette comprising a protease inhibitor polynucleotide operably linked to a promoter; (b) growing the plant cell under plant growing conditions; and  
25 (c) inducing expression of the polynucleotide .

## **DETAILED DESCRIPTION**

### **Figure listing**

Figure 1 Protease Inhibition

### 5    **Sequence identification**

Barley High Lysine 1(BHL-1) is coded for by the polypeptides of SEQ ID No. 2 which is encoded for by the nucleic acid of SEQ ID No. 1.

Barley High Lysine 2 (BHL-2) is coded for by the polypeptides of SEQ ID No. 4 which is encoded for by the nucleic acid of SEQ ID No. 3.

10        Barley High Lysine 3 (BHL-3) is coded for by the polypeptides of SEQ ID No. 6 which is encoded for by the nucleic acid of SEQ ID No. 5.

Barley High Lysine 3N (BHL-3N) is coded for by the polypeptides of SEQ ID No. 8 which is encoded for by the nucleic acid of SEQ ID No. 7.

15        Barley High Lysine 1N (BHL-1N) is coded for by the polypeptides of SEQ ID No. 10 which is encoded for by the nucleic acid of SEQ ID No. 9.

Barley High Lysine 2N (BHL-2N) is coded for by the polypeptides of SEQ ID No. 12 which is encoded for by the nucleic acid of SEQ ID No. 11.

20        Wild-type chymotrypsin inhibitor (WI-CI-2) is coded for by the polypeptides of SEQ ID No. 14 which is encoded for by the nucleic acid of SEQ ID No. 13.

Maize EST PI-1 is coded for by the polypeptides of SEQ ID No.16 which is encoded for by the nucleic acid of SEQ ID No. 15.

Maize EST PI-2 is coded for by the polypeptides of SEQ ID No.18 which is encoded for by the nucleic acid of SEQ ID No. 17.

25        Maize EST PI-3 is coded for by the polypeptides of SEQ ID No.20 which is encoded for by the nucleic acid of SEQ ID No. 19.

Maize EST PI-4 is coded for by the polypeptides of SEQ ID No.22 which is encoded for by the nucleic acid of SEQ ID No. 21.

30        Maize EST PI-5 is coded for by the polypeptides of SEQ ID No. 24 which is encoded for by the nucleic acid of SEQ ID No. 23.

The 5' and 3' PCR primer pairs A & B, are identified as SEQ ID Nos. 25 and 26, respectively.

### **Definitions**

Units, prefixes, and symbols may be denoted in their SI accepted form. Unless  
5 otherwise indicated, nucleic acids are written left to right in 5' to 3' orientation; amino  
acid sequences are written left to right in amino to carboxy orientation, respectively.  
Numeric ranges are inclusive of the numbers defining the range. Amino acids may be  
referred to herein by either their commonly known three letter symbols or by the one-  
letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature  
10 Commission. Nucleotides, likewise, may be referred to by their commonly accepted  
single-letter codes. The terms defined below are more fully defined by reference to the  
specification as a whole.

“Chymotrypsin inhibitor-like” protein is a protein with a sequence identity of 40%  
or more to the CI-2 from barley.

15 “%” refers to molar % unless otherwise specified or implied.

“Essential amino acids” are amino acids that must be obtained from an external  
source because they are not synthesized by the individual. They are comprised of:  
methionine, threonine, lysine, isoleucine, leucine, valine, tryptophan, phenylalanine, and  
histidine.

20 By “binding partner” or “interacting molecule” it is intended a molecule which is  
capable of binding or interacting with the proteins of interest. Such binding partners or  
interacting molecules include antibodies, monoclonal antibodies, antibody fragments,  
proteins, modified proteins, nucleotide sequences, aptamers, chemical compounds (e.g.  
carbohydrates, etc.), or combinations thereof.

25 By “amplified” is meant the construction of multiple copies of a nucleic acid  
sequence or multiple copies complementary to the nucleic acid sequence using at least  
one of the nucleic acid sequences as a template. Amplification systems include the  
polymerase chain reaction (PCR) system, ligase chain reaction (LCR) system, nucleic  
acid sequence based amplification (NASBA, Cangene, Mississauga, Ontario), Q-Beta  
30 Replicase systems, transcription-based amplification system (TAS), and strand  
displacement amplification (SDA). See, e.g., *Diagnostic Molecular Microbiology*:

*Principles and Applications*, D. H. Persing *et al.*, Ed., American Society for Microbiology, Washington, D.C. (1993).

The term "antibody" includes reference to antigen binding forms of antibodies (e.g., Fab, F(ab)<sub>2</sub>). The term "antibody" refers to a polypeptide substantially encoded by an immunoglobulin gene or immunoglobulin genes, or fragments thereof which specifically bind and recognize an analyte (antigen). While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized *de novo* either chemically or by utilizing recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments such as single chain Fv, chimeric antibodies (i.e., comprising constant and variable regions from different species), humanized antibodies (i.e., comprising a complementarity determining region (CDR) from a non-human source) and heteroconjugate antibodies (e.g., bispecific antibodies).

The term "antigen" includes reference to a substance to which an antibody can be generated and/or to which the antibody is specifically immunoreactive. The specific immunoreactive sites within the antigen are known as epitopes or antigenic determinants. These may be a linear array of amino acids or of a more complex secondary or tertiary structure. Those of skill will recognize that all immunogens (i.e., substance capable of eliciting an immune response) are antigens; however some antigens, such as haptens, are not immunogens but may be made immunogenic by coupling to a carrier molecule. An antibody immunologically reactive with a particular antigen can be generated *in vivo* or by recombinant methods such as selection of libraries of recombinant antibodies in phage or similar vectors. *See, e.g., Huse et al., Science* 246: 1275-1281 (1989); and Ward, *et al., Nature* 341: 544-546 (1989); and Vaughan *et al., Nature Biotech.* 14: 309-314 (1996).

As used herein, "antisense orientation" includes reference to a duplex polynucleotide sequence which is operably linked to a promoter in an orientation where the antisense strand is transcribed. The antisense strand is sufficiently complementary to an endogenous transcription product such that translation of the endogenous transcription product is often inhibited.

As used herein, "chromosomal region" includes reference to a length of chromosome which may be measured by reference to the linear segment of DNA which it

comprises. The chromosomal region can be defined by reference to two unique DNA sequences, i.e., markers.

The term "conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode any given protein. For instance, the codons GCA, GCC, GCG and GCU all encode the amino acid alanine. Thus, at every position where an alanine is specified by a codon, the codon can be altered to any of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations" and represent one species of conservatively modified variation. Every nucleic acid sequence herein which encodes a polypeptide also describes every possible silent variation of the nucleic acid. One of ordinary skill will recognize that each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, each silent variation of a nucleic acid which encodes a polypeptide of the present invention is implicit in each described polypeptide sequence and incorporated herein by reference.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Thus, any number of amino acid residues selected from the group of integers consisting of from 1 to 15 can be so altered. Thus, for example, 1, 2, 3, 4, 5, 7, or 10 alterations can be made. Conservatively modified variants typically provide similar biological activity as the unmodified polypeptide sequence from which they are derived. For example, substrate specificity, enzyme activity, or ligand/receptor binding is generally at least 30%, 40%, 50%, 60%, 70%, 80%, or 90% of the native protein for its native substrate.



Conservative substitution tables providing functionally similar amino acids are well known in the art.

The following six groups each contain amino acids that are conservative substitutions for one another:

- 5 1) Alanine (A), Serine (S), Threonine (T);
- 2) Aspartic acid (D), Glutamic acid (E);
- 3) Asparagine (N), Glutamine (Q);
- 4) Arginine (R), Lysine (K);
- 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); and
- 10 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W).

See also, Creighton (1984) *Proteins* W.H. Freeman and Company.

By "encoding" or "encoded", with respect to a specified nucleic acid, is meant comprising the information for translation into the specified protein. A nucleic acid encoding a protein may comprise non-translated sequence (e.g., introns) within translated  
 15 regions of the nucleic acid, or may lack such intervening non-translated sequences (e.g., as in cDNA). The information by which a protein is encoded is specified by the use of codons. Typically, the amino acid sequence is encoded by the nucleic acid using the "universal" genetic code. However, variants of the universal code, such as is present in some plant, animal, and fungal mitochondria, the bacterium *Mycoplasma capricolum*  
 20 (Proc. Natl. Acad. Sci. (USA), 82: 2306-2309 (1985)), or the ciliate *Macronucleus*, may be used when the nucleic acid is expressed using these organisms.

When the nucleic acid is prepared or altered synthetically, advantage can be taken of known codon preferences of the intended host where the nucleic acid is to be expressed. For example, although nucleic acid sequences of the present invention may be  
 25 expressed in both monocotyledonous and dicotyledonous plant species, sequences can be modified to account for the specific codon preferences and GC content preferences of monocotyledons or dicotyledons as these preferences have been shown to differ (Murray *et al.* *Nucl. Acids Res.* 17: 477-498 (1989)). Thus, the maize preferred codon for a particular amino acid may be derived from known gene sequences from maize. Maize  
 30 codon usage for 28 genes from maize plants are listed in Table 4 of Murray *et al.*, *supra*.

As used herein "full-length sequence" includes reference to a protease inhibitor polynucleotide or the encoded protein having the entire amino acid sequence of, a native

(non-synthetic), endogenous, catalytically active form of a protein involved in protease inhibition. A full-length sequence can be determined by size comparison relative to a control which is a native (non-synthetic) endogenous cellular protease inhibitor nucleic acid or protein. Methods to determine whether a sequence is full-length are well known  
5 in the art including such exemplary techniques as northern or western blots. See, e.g., *Plant Molecular Biology: A Laboratory Manual*, Clark, Ed., Springer-Verlag, Berlin (1997). Comparison to known full-length homologous sequences can also be used to identify full-length sequences of the present invention. Additionally, consensus sequences typically present at the 5' and 3' untranslated regions of mRNA aid in the  
10 identification of a polynucleotide as full-length. For example, the consensus sequence ANNNNAAUGG, where the underlined codon represents the N-terminal methionine, aids in determining whether the polynucleotide has a complete 5' end. Consensus sequences at the 3' end, such as polyadenylation sequences, aid in determining whether the polynucleotide has a complete 3' end.

15 As used herein, "heterologous" in reference to a nucleic acid is a nucleic acid that originates from a foreign species, or, if from the same species, is substantially modified from its native form in composition and/or genomic locus. For example, a promoter operably linked to a heterologous structural gene is from a species different from that from which the structural gene was derived, or, if from the same species, one or both are  
20 substantially modified from their original form. A heterologous protein may originate from a foreign species or, if from the same species, is substantially modified from its original form.

By "host cell" is meant a cell which contains a vector and supports the replication and/or expression of the expression vector. Host cells may be prokaryotic cells such as *E.*  
25 *coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells. Preferably, host cells are monocotyledonous or dicotyledonous plant cells. A particularly preferred monocotyledonous host cell is a maize host cell.

The term "hybridization complex" includes reference to a duplex nucleic acid sequence formed by two single-stranded nucleic acid sequences which selectively  
30 hybridize with each other.

By "immunologically reactive conditions" is meant conditions which allow an antibody, generated to a particular epitope, to bind to that epitope to a detectably greater

degree (e.g., at least 2-fold over background) than the antibody binds to substantially all other epitopes. Immunologically reactive conditions are dependent upon the format of the antibody binding reaction and typically are those utilized in immunoassay protocols. See Harlow and Lane, *Antibodies, A Laboratory Manual*, Cold Spring Harbor Publications, New York (1988), for a description of immunoassay formats and conditions.

The terms "isolated" or "biologically pure" refer to material which is: (1) substantially or essentially free from components which normally accompany or interact with it as found in its naturally occurring environment. The isolated material optionally comprises material not found with the material in its natural environment. (2) If the material is in its natural environment, the material has been synthetically (non-naturally) altered to a composition and/or placed at a locus in the cell (e.g., genome) not native to a material found in that environment. The alteration to yield the synthetic material can be performed on the material within or removed from its natural state. For example, a naturally occurring nucleic acid becomes an isolated nucleic acid if it is altered, or if it is transcribed from DNA which is altered, by non-natural, synthetic (i.e., "man-made") methods performed within the cell from which it originates. See, e.g., Compounds and Methods for Site Directed Mutagenesis in Eukaryotic Cells, Kmiec, U.S. Patent No. 5,565,350; *In Vivo* Homologous Sequence Targeting in Eukaryotic Cells; Zarling *et al.*, PCT/US93/03868. Likewise, a naturally occurring nucleic acid (e.g., a promoter) become isolated if it is introduced by non-naturally occurring means to a locus of the genome not native to that nucleic acid.

The term "protease inhibitor nucleic acids" means an isolated nucleic acid comprising a polynucleotide (a "protease inhibitor polynucleotide") encoding a polypeptide involved in protease inhibition.

As used herein, "localized within the chromosomal region defined by and including" with respect to particular markers includes reference to a contiguous length of a chromosome delimited by and including the stated markers.

As used herein, "marker" includes reference to a locus on a chromosome that serves to identify a unique position on the chromosome. A "polymorphic marker" includes reference to a marker which appears in multiple forms (alleles) such that different forms of the marker, when they are present in a homologous pair, allow

transmission of each of the chromosomes in that pair to be followed. A genotype may be defined by use of a single or a plurality of markers.

As used herein, "nucleic acid" includes reference to a deoxyribonucleotide or ribonucleotide polymer in either single- or double-stranded form, and unless otherwise  
5 limited, encompasses known analogues of natural nucleotides that hybridize to single-stranded nucleic acids in a manner similar to naturally occurring nucleotides (e.g., peptide nucleic acids).

By "nucleic acid library" is meant a collection of isolated DNA or RNA molecules which comprise and substantially represent the entire transcribed fraction of a genome of  
10 a specified organism. Construction of exemplary nucleic acid libraries, such as genomic and cDNA libraries, is taught in standard molecular biology references such as Berger and Kimmel, *Guide to Molecular Cloning Techniques, Methods in Enzymology*, Vol. 152, Academic Press, Inc., San Diego, CA (Berger); Sambrook *et al.*, *Molecular Cloning - A Laboratory Manual*, 2nd ed., Vol. 1-3 (1989); and *Current Protocols in Molecular*  
15 *Biology*, F.M. Ausubel *et al.*, Eds., Current Protocols, a joint venture between Greene Publishing Associates, Inc. and John Wiley & Sons, Inc. (1994 Supplement).

As used herein "operably linked" includes reference to a functional linkage between a promoter and a second sequence, wherein the promoter sequence initiates and mediates transcription of the DNA sequence corresponding to the second sequence.  
20 Generally, operably linked means that the nucleic acid sequences being linked are contiguous and, where necessary to join two protein coding regions, contiguous and in the same reading frame.

As used herein, the term "plant" includes reference to whole plants, plant organs (e.g., leaves, stems, roots, etc.), seeds and plant cells and progeny of same. Plant cell, as  
25 used herein includes, without limitation, seeds suspension cultures, embryos, meristematic regions, callus tissue, leaves, roots, shoots, gametophytes, sporophytes, pollen, and microspores. The class of plants which can be used in the methods of the invention is generally as broad as the class of higher plants amenable to transformation techniques, including both monocotyledonous and  
30 dicotyledonous plants. Particularly preferred is *Zea mays*.

As used herein, "polynucleotide" includes reference to a deoxyribopolynucleotide, ribopolynucleotide, or analogs thereof, that hybridize to nucleic acids in a manner similar

to naturally occurring nucleotides. A polynucleotide can be full-length or a sub-sequence of a native or heterologous structural or regulatory gene. Unless otherwise indicated, the term includes reference to the specified sequence as well as the complementary sequence thereof. Thus, DNAs or RNAs with backbones modified for stability or for other reasons are

5 "polynucleotides" as that term is intended herein. Moreover, DNAs or RNAs comprising unusual bases, such as inosine, or modified bases, such as tritylated bases, to name just two examples, are polynucleotides as the term is used herein. It will be appreciated that a great variety of modifications have been made to DNA and RNA that serve many useful purposes known to those of skill in the art. The term polynucleotide as it is employed herein

10 embraces such chemically, enzymatically or metabolically modified forms of polynucleotides, as well as the chemical forms of DNA and RNA characteristic of viruses and cells, including *inter alia*, simple and complex cells.

The terms "polypeptide", "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in

15 which one or more amino acid residue is an artificial chemical analogue of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers. Among the known modifications which may be present in polypeptides of the present are, to name an illustrative few, acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent

20 attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cystine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, proteolytic

25 processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. Such modifications are well known to those of skill and have been described in great detail in the scientific literature. Several particularly common modifications, glycosylation, lipid attachment, sulfation, gamma-carboxylation of glutamic acid residues, hydroxylation and

30 ADP-ribosylation, for instance, are described in most basic texts, such as, for instance *Proteins - Structure and Molecular Properties*, 2nd ed., T. E. Creighton, W. H. Freeman and Company, New York (1993). Many detailed reviews are available on this subject, such

as, for example, those provided by Wold, F., *Posttranslational Protein Modifications: Perspectives and Prospects*, pp. 1-12 in *Posttranslational Covalent Modification of Proteins*, B. C. Johnson, Ed., Academic Press, New York (1983); Seifter *et al.*, *Meth. Enzymol.* 182: 626-646 (1990) and Rattan *et al.*, *Protein Synthesis: Posttranslational Modifications and Aging*, *Ann. N.Y. Acad. Sci.* 663: 48-62 (1992). It will be appreciated, as is well known and as noted above, that polypeptides are not always entirely linear. For instance, polypeptides may be branched as a result of ubiquitination, and they may be circular, with or without branching, generally as a result of posttranslation events, including natural processing event and events brought about by human manipulation which do not occur naturally. Circular, branched and branched circular polypeptides may be synthesized by non-translation natural process and by entirely synthetic methods, as well. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. In fact, blockage of the amino or carboxyl group in a polypeptide, or both, by a covalent modification, is common in naturally occurring and synthetic polypeptides and such modifications may be present in polypeptides of the present invention, as well. For instance, the amino terminal residue of polypeptides made in *E. coli* or other cells, prior to proteolytic processing, almost invariably will be N-formylmethionine. During post-translational modification of the peptide, a methionine residue at the NH<sub>2</sub>-terminus may be deleted. Accordingly, this invention contemplates the use of both the methionine-containing and the methionineless amino terminal variants of the protein of the invention. In general, as used herein, the term polypeptide encompasses all such modifications, particularly those that are present in polypeptides synthesized by expressing a polynucleotide in a host cell.

As used herein "promoter" includes reference to a region of DNA upstream from the start of transcription and involved in recognition and binding of RNA polymerase and other proteins to initiate transcription. A "plant promoter" is a promoter capable of initiating transcription in plant cells. Examples of promoters under developmental control include promoters that preferentially initiate transcription in certain tissues, such as leaves, roots, seeds, fibers, xylem vessels, tracheids, or sclerenchyma. Such promoters are referred to as "tissue preferred". Promoters which initiate transcription only in certain tissue are referred to as "tissue specific". A "cell type" specific promoter is primarily drives expression in certain cell types in one or more organs, for example, vascular cells

in roots or leaves. An "inducible" promoter is a promoter which is under environmental control. Examples of environmental conditions that may effect transcription by inducible promoters include anaerobic conditions or the presence of light. Tissue specific, cell type specific, and inducible promoters constitute the class of "non-constitutive" promoters. A  
5 "constitutive" promoter is a promoter which is active under most environmental conditions.

The terms "polypeptide involved in protease inhibition" or "protease inhibitor polypeptide" refer to one or more proteins, in glycosylated or non-glycosylated form, acting as a protease inhibitor. Examples are included as, but not limited to: chymotrypsin  
10 inhibitor, trypsin inhibitor, protease inhibitor, pre-pro-proteinase inhibitor I, subtilisin-chymotrypsin inhibitor, tumor-related protein, genetic tumor-related proteinase inhibitor, subtilisin inhibitor, endopeptidase inhibitor, serine protease inhibitor, wound-inducible proteinase inhibitor, and eglin c. The term is also inclusive of fragments, variants, homologs, alleles or precursors (e.g., preproteins or proproteins) thereof. A "protease  
15 inhibitor protein" comprises a protease inhibitor polypeptide.

As used herein "recombinant" includes reference to a cell, or nucleic acid, or vector, that has been modified by the introduction of a heterologous nucleic acid or the alteration or placement of a native nucleic acid to a form or to a locus not native to that cell, or that the cell is derived from a cell so modified. Thus, for example, recombinant  
20 cells express genes that are not found in identical form within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed or not expressed at all. The term "recombinant" as used herein does not encompass the alteration of the cell, nucleic acid or vector by naturally occurring events (e.g., spontaneous mutation, natural  
25 transformation/transduction/transposition) such as those occurring without direct human intervention.

As used herein, a "recombinant expression cassette" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements which permit transcription of a particular nucleic acid in a target cell. The recombinant  
30 expression cassette can be incorporated into a plasmid, chromosome, mitochondrial DNA, plastid DNA, virus, or nucleic acid fragment. Typically, the recombinant expression

cassette portion of the expression vector includes, among other sequences, a nucleic acid to be transcribed, and a promoter.

The term "residue" or "amino acid residue" or "amino acid" are used interchangeably herein to refer to an amino acid that is incorporated into a protein, polypeptide, or peptide (collectively "protein"). The amino acid may be a naturally occurring amino acid and, unless otherwise limited, may encompass known analogs of natural amino acids that can function in a similar manner as naturally occurring amino acids.

The term "selectively hybridizes" includes reference to hybridization, under stringent hybridization conditions, of a nucleic acid sequence to a specified nucleic acid target sequence to a detectably greater degree (e.g., at least 2-fold over background) than its hybridization to non-target nucleic acid sequences and to the substantial exclusion of non-target nucleic acids. Selectively hybridizing sequences typically have about at least 80% sequence identity, preferably 90% sequence identity, and most preferably 100% sequence identity (i.e., complementary) with each other.

The term "specifically reactive", includes reference to a binding reaction between an antibody and a protein having an epitope recognized by the antigen binding site of the antibody. This binding reaction is determinative of the presence of a protein having the recognized epitope amongst the presence of a heterogeneous population of proteins and other biologics. Thus, under designated immunoassay conditions, the specified antibodies bind to an analyte having the recognized epitope to a substantially greater degree (e.g., at least 2-fold over background) than to substantially all other analytes lacking the epitope which are present in the sample.

Specific binding to an antibody under such conditions may require an antibody that is selected for its specificity for a particular protein. For example, antibodies raised to the polypeptides involved in protease inhibition can be selected from to obtain antibodies specifically reactive with polypeptides involved in protease inhibition. The proteins used as immunogens can be in native conformation or denatured so as to provide a linear epitope.

A variety of immunoassay formats may be used to select antibodies specifically reactive with a particular protein (or other analyte). For example, solid-phase ELISA immunoassays are routinely used to select monoclonal antibodies specifically



immunoreactive with a protein. See Harlow and Lane, *Antibodies, A Laboratory Manual*, Cold Spring Harbor Publications, New York (1988), for a description of immunoassay formats and conditions that can be used to determine selective reactivity.

The terms "stringent conditions" or "stringent hybridization conditions" includes  
5 reference to conditions under which a probe will hybridize to its target sequence, to a detectably greater degree than other sequences (e.g., at least 2-fold over background). Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. Generally, stringent conditions are selected to be about 5 °C lower than the thermal  
10 melting point ( $T_m$ ) for the specific sequence at a defined ionic strength and pH. The  $T_m$  is the temperature (under defined ionic strength and pH) at which 50% of a complementary target sequence hybridizes to a perfectly matched probe. Typically, stringent conditions will be those in which the salt concentration is less than about 1.0 M Na ion, typically about 0.01 to 1.0 M Na ion concentration (or other salts) at pH 7.0 to 8.3 and the  
15 temperature is at least about 30°C for short probes (e.g., 10 to 50 nucleotides) and at least about 60°C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. Exemplary low stringency conditions include hybridization with a buffer solution of 30% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 2X SSC at 50°C. Exemplary high stringency  
20 conditions include hybridization in 50% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 0.1X SSC at 60°C.

Stringent hybridization conditions in the context of nucleic acid hybridization assay formats are sequence dependent, and are different under different environmental parameters. Longer sequences hybridize selectively at higher temperatures. An extensive  
25 guide to the hybridization of nucleic acids is found in Tijssen, *Laboratory Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Acid Probes*, Part I, Chapter 2 "Overview of principles of hybridization and the strategy of nucleic acid probe assays", Elsevier, New York (1993).

The terms "transfection" or "transformation" include reference to the introduction  
30 of a nucleic acid into a eukaryotic or prokaryotic cell where the nucleic acid may be incorporated into the genome of the cell (e.g., chromosome, plasmid, plastid or

mitochondrial DNA), converted into an autonomous replicon, or transiently expressed (e.g., transfected mRNA).

As used herein, "transgenic plant" includes reference to a plant which comprises within its genome a heterologous polynucleotide. Generally, the heterologous polynucleotide is stably integrated within the genome such that the polynucleotide is passed on to successive generations. The heterologous polynucleotide may be integrated into the genome alone or as part of a recombinant expression cassette. "Transgenic" is used herein to include any cell, cell line, callus, tissue, plant part or plant, the genotype of which has been altered by the presence of heterologous nucleic acid including those transgenics initially so altered as well as those created by sexual crosses or asexual propagation from the initial transgenic. The term "transgenic" as used herein does not encompass the alteration of the genome (chromosomal or extra-chromosomal) by conventional plant breeding methods or by naturally occurring events such as random cross-fertilization, non-recombinant viral infection, non-recombinant bacterial transformation, non-recombinant transposition, or spontaneous mutation.

As used herein, "vector" includes reference to a nucleic acid used in transfection of a host cell and into which can be inserted a polynucleotide. Vectors are often replicons. Expression vectors permit transcription of a nucleic acid inserted therein.

The following terms are used to describe the sequence relationships between two or more nucleic acids or polynucleotides: (a) "reference sequence", (b) "comparison window", (c) "sequence identity", (d) "percentage of sequence identity", and (e) "substantial identity".

(a) As used herein, "reference sequence" is a defined sequence used as a basis for sequence comparison. A reference sequence may be a subset or the entirety of a specified sequence; for example, as a segment of a full-length cDNA or gene sequence, or the complete cDNA or gene sequence.

(b) As used herein, "comparison window" means includes reference to a contiguous and specified segment of a polynucleotide sequence, wherein the polynucleotide sequence may be compared to a reference sequence and wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) compared to the reference sequence (which does not

comprise additions or deletions) for optimal alignment of the two sequences. Generally, the comparison window is at least 20 contiguous nucleotides in length, and optionally can be 30, 40, 50, 100, or longer. Those of skill in the art understand that to avoid a high similarity to a reference sequence due to inclusion of gaps in the polynucleotide sequence  
5 a gap penalty is typically introduced and is subtracted from the number of matches.

Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison may be conducted by the local homology algorithm of Smith and Waterman, Adv. Appl. Math. 2: 482 (1981); by the homology alignment algorithm of Needleman and Wunsch, J. Mol. Biol. 48: 443 (1970); by the  
10 search for similarity method of Pearson and Lipman, Proc. Natl. Acad. Sci. 85: 2444 (1988); by computerized implementations of these algorithms, including, but not limited to: CLUSTAL in the PC/Gene program by Intelligenetics, Mountain View, California, GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, Wisconsin, USA;  
15 the CLUSTAL program is well described by Higgins and Sharp, Gene 73: 237-244 (1988); Higgins and Sharp, CABIOS 5: 151-153 (1989); Corpet, *et al.*, Nucleic Acids Research 16: 10881-90 (1988); Huang, *et al.*, Computer Applications in the Biosciences 8: 155-65 (1992), and Pearson, *et al.*, Methods in Molecular Biology 24: 307-331 (1994); preferred computer alignment methods also include the BLASTP, BLASTN, and  
20 BLASTX algorithms. Altschul, *et al.*, J. Mol. Biol. 215: 403-410 (1990). Alignment is also often performed by inspection and manual alignment.

(c) As used herein, "sequence identity" or "identity" in the context of two nucleic acid or polypeptide sequences includes reference to the residues in the two sequences which are the same when aligned for maximum correspondence over a  
25 specified comparison window. When percentage of sequence identity is used in reference to proteins it is recognized that residue positions which are not identical often differ by conservative amino acid substitutions, where amino acid residues are substituted for other amino acid residues with similar chemical properties (e.g. charge or hydrophobicity) and therefore do not change the functional properties of the molecule. Where sequences differ  
30 in conservative substitutions, the percent sequence identity may be adjusted upwards to correct for the conservative nature of the substitution. Sequences which differ by such conservative substitutions are said to have "sequence similarity" or "similarity". Means

for making this adjustment are well-known to those of skill in the art. Typically this involves scoring a conservative substitution as a partial rather than a full mismatch, thereby increasing the percentage sequence identity. Thus, for example, where an identical amino acid is given a score of 1 and a non-conservative substitution is given a score of zero, a conservative substitution is given a score between zero and 1. The scoring of conservative substitutions is calculated, *e.g.*, according to the algorithm of Meyers and Miller, Computer Applic. Biol. Sci., 4: 11-17 (1988) *e.g.*, as implemented in the program PC/GENE (Intelligenetics, Mountain View, California, USA).

(d) As used herein, "percentage of sequence identity" means the value determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity.

(e) (i) The term "substantial identity" of polynucleotide sequences means that a polynucleotide comprises a sequence that has at least 70% sequence identity, preferably at least 80%, more preferably at least 90% and most preferably at least 95%, compared to a reference sequence using one of the alignment programs described using standard parameters. One of skill will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning and the like. Substantial identity of amino acid sequences for these purposes normally means sequence identity of at least 60%, more preferably at least 70%, 80%, 90%, and most preferably at least 95%. Polypeptides which are "substantially similar" share sequences as noted above except that residue positions which are not identical may differ by conservative amino acid changes.

Another indication that nucleotide sequences are substantially identical is if two molecules hybridize to each other under stringent conditions. Generally, stringent

conditions are selected to be about 5°C to about 20°C lower than the thermal melting point ( $T_m$ ) for the specific sequence at a defined ionic strength and pH. The  $T_m$  is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Typically, stringent wash conditions are those in which the salt concentration is about 0.02 molar at pH 7 and the temperature is at least about 50, 55, or 60°C. However, nucleic acids which do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This may occur, *e.g.*, when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. One indication that two nucleic acid sequences are substantially identical is that the polypeptide which the first nucleic acid encodes is immunologically cross reactive with the polypeptide encoded by the second nucleic acid.

(e) (ii) The terms "substantial identity" in the context of a peptide indicates that a peptide comprises a sequence with at least 70% sequence identity to a reference sequence, preferably 80%, more preferably 85%, most preferably at least 90% or 95% sequence identity to the reference sequence over a specified comparison window. Preferably, optimal alignment is conducted using the homology alignment algorithm of Needleman and Wunsch, J. Mol. Biol. 48: 443 (1970). An indication that two peptide sequences are substantially identical is that one peptide is immunologically reactive with antibodies raised against the second peptide. Thus, a peptide is substantially identical to a second peptide, for example, where the two peptides differ only by a conservative substitution.

It has been unexpectedly discovered that a protease inhibitor can be modified to enhance its content of essential amino acids coupled with reduction in protease inhibitor activity. In a preferred embodiment of the present invention, derivatives of the protease inhibitor, CI-2, simultaneously exhibit both enhanced essential amino acid content as well as decreased protease inhibitor activity. The present compounds are thus excellent candidates for enhancing the nutritional value of feed.

The present invention provides, *inter alia*, compositions and methods for modulating (i.e., increasing or decreasing) the total levels of essential amino acids and/or

altering the ratios of essential amino acids in plants. Thus, the present invention provides utility in such exemplary applications as improving the nutritional properties of fodder crops, increasing the value of plant material for pulp and paper production, altering the protease inhibitory activity, as well as for improving the utility of plant material where the amount of essential amino acids or composition is important, such as the use of plant as a feed. In particular, protease inhibitor polypeptides may be expressed at times or in quantities which are not characteristic of natural plants.

The present invention also provides isolated nucleic acid comprising polynucleotides of sufficient length and complementarity to a protease inhibitor gene, to use as probes or amplification primers in the detection, quantitation, or isolation of gene transcripts. For example, isolated nucleic acids of the present invention can be used as probes in detecting deficiencies in the level of mRNA in screenings for desired transgenic plants, for detecting mutations in the gene (e.g., substitutions, deletions, or additions), for monitoring upregulation of protease inhibition in screening assays for compounds affecting protease inhibition, or for use as molecular markers in plant breeding programs. The isolated nucleic acids of the present invention can also be used for recombinant expression of protease inhibitor polypeptides for use as immunogens in the preparation and/or screening of antibodies. The isolated nucleic acids of the present invention can also be employed for use in sense or antisense suppression of one or more protease inhibitor genes in a host cell, tissue, or plant. Further, using a primer specific to an insertion sequence (e.g., transposon) and a primer which specifically hybridizes to an isolated nucleic acid of the present invention, one can use nucleic acid amplification to identify insertion sequence inactivated protease inhibitor genes from a cDNA library prepared from insertion sequence mutagenized plants. Progeny seed from the plants comprising the desired inactivated gene can be grown to a plant to study the phenotypic changes characteristic of that inactivation. See, *Tools to Determine the Function of Genes*, 1995 Proceedings of the Fiftieth Annual Corn and Sorghum Industry Research Conference, American Seed Trade Association, Washington, D.C., 1995.

The present invention also provides isolated proteins comprising polypeptides having a minimal amino acid sequence from the polypeptides involved in protease inhibition as disclosed herein. The present invention also provides proteins comprising at least one epitope from a polypeptide involved in protease inhibition. The proteins of the

present invention can be employed in assays for enzyme agonists or antagonists of enzyme function, or for use as immunogens or antigens to obtain antibodies specifically immunoreactive with a protein of the present invention. Such antibodies can be used in assays for expression levels, for identifying and/or isolating nucleic acids of the present invention from expression libraries, or for purification of polypeptides involved in protease inhibition. In a preferred embodiment of the present invention, the present protein has both elevated essential amino acid content and reduced protease inhibitor activity.

The isolated nucleic acids of the present invention can be used over a broad range of plant types, including species from the genera *Cucurbita*, *Rosa*, *Vitis*, *Juglans*, *Fragaria*, *Lotus*, *Medicago*, *Onobrychis*, *Trifolium*, *Trigonella*, *Vigna*, *Citrus*, *Linum*, *Geranium*, *Manihot*, *Daucus*, *Arabidopsis*, *Brassica*, *Raphanus*, *Sinapis*, *Atropa*, *Capsicum*, *Datura*, *Hyoscyamus*, *Lycopersicon*, *Nicotiana*, *Solanum*, *Petunia*, *Digitalis*, *Majorana*, *Ciahorium*, *Helianthus*, *Lactuca*, *Bromus*, *Asparagus*, *Antirrhinum*, *Heterocallis*, *Nemesis*, *Pelargonium*, *Panieum*, *Pennisetum*, *Ranunculus*, *Senecio*, *Salpiglossis*, *Cucumis*, *Browaalia*, *Glycine*, *Pisum*, *Phaseolus*, *Lolium*, *Oryza*, *Zea*, *Avena*, *Hordeum*, *Secale*, *Triticum*, *Sorghum*, *Picea*, and *Populus*.

The isolated nucleic acids of the present invention can be used over a broad range of polypeptide types, including anti microbial peptides such as those described and incorporated by reference in Rao, G., Antimicrobial Peptides; Molecular Plant-Microbe Interactions 8: 6-13 (1995).

### **Protease Inhibitor Nucleic Acids**

The present invention provides, *inter alia*, isolated and/or heterologous nucleic acids of RNA, DNA, and analogs and/or chimeras thereof, comprising a protease inhibitor polynucleotide encoding such proteins as: chymotrypsin inhibitor, trypsin inhibitor, protease inhibitor, pre-pro-proteinase inhibitor I, subtilisin-chymotrypsin inhibitor, tumor-related protein, genetic tumor-related proteinase inhibitor, subtilisin inhibitor,

endopeptidase inhibitor, serine protease inhibitor, wound-inducible proteinase inhibitor, and eglin c. The protease inhibitor nucleic acids of the present invention comprise protease inhibitor polynucleotides which, are inclusive of:

(a) a polynucleotide encoding a protease inhibitor polypeptide of SEQ ID NOS: 2,4,6,8,10, or 12,16,18,20,22,24 and conservatively modified and polymorphic variants thereof, including exemplary polynucleotides of SEQ ID NOS: 1,3,5,7,9 and 11, 15,17,19,21, 23 and conservative changes

(b) a polynucleotide which is the product of amplification from a *Zea mays* nucleic acid library using primer pairs from amongst the consecutive pairs from SEQ ID NOS: 25 and 26, which amplify polynucleotides having substantial identity to polynucleotides from amongst those having SEQ ID NOS: 1,3,5,7,9 or 11,15,17,19,21, 23

(c) a polynucleotide which selectively hybridizes to a polynucleotide of (a) or (b);

(d) a polynucleotide having at least 60% sequence identity with polynucleotides of (a), (b), or (c);

(e) a polynucleotide encoding a protein having a specified number of contiguous amino acids from a prototype polypeptide, wherein the protein is specifically recognized by antisera elicited by presentation of the protein and wherein the protein does not detectably immunoreact to antisera which has been fully immunosorbed with the protein;

(f) complementary sequences of polynucleotides of (a), (b), (c), (d), or (e); and

(g) a polynucleotide comprising at least 15 contiguous nucleotides from a polynucleotide of (a), (b), (c), (d), (e), or (f).

#### *A. Polynucleotides Encoding A Protease inhibitor Protein of SEQ ID NOS: 2,4,6,8,10 and 12,16,18,20,22,24 or Conservatively Modified or Polymorphic Variants Thereof*

As indicated in (a), *supra*, the present invention provides isolated and/or heterologous nucleic acids comprising protease inhibitor polynucleotides, wherein the polynucleotides encode the protease inhibitor polypeptides disclosed herein as SEQ ID NOS: 2,4,6,8,10 and 12,16,18,20,22,24 or conservatively modified or polymorphic variants thereof. Those of skill in the art will recognize that the degeneracy of the genetic



code allows for a plurality of polynucleotides to encode for the identical amino acid sequence. Thus, the present invention includes protease inhibitor polynucleotides of SEQ ID NOS: 1,3,5,7,9 and 11, 15,17,19,21, 23 and silent variations of polynucleotides encoding a protease inhibitor polypeptide of SEQ ID NOS: 2,4,6,8,10 and  
5 12,16,18,20,22,24. The present invention further provides isolated and/or heterologous nucleic acids comprising protease inhibitor polynucleotides encoding conservatively modified variants of a protease inhibitor polypeptide of SEQ ID NOS: 2,4,6,8,10 and 12, 16,18,20,22,24. Additionally, the present invention further provides isolated and/or heterologous nucleic acids comprising protease inhibitor polynucleotides encoding one or  
10 more polymorphic (allelic) variants of protease inhibitor polypeptides/polynucleotides.

*B. Polynucleotides Amplified from a Zea mays Nucleic Acid Library*

As indicated in (b), *supra*, the present invention provides isolated and/or heterologous nucleic acids comprising protease inhibitor polynucleotides, wherein the  
15 polynucleotides are amplified from a *Zea mays* nucleic acid library. The nucleic acid library may be a cDNA library, a genomic library, or a library generally constructed from nuclear transcripts at any stage of intron processing. Nucleic acid libraries from other plants, both monocots and dicots could also be used in a similar fashion. The polynucleotides of the present invention include those amplified using the following  
20 primer pairs:

SEQ ID NOS: 25 and 26 which yield an amplicon comprising a sequence having substantial identity to SEQ ID NOS: 7,9, and 11.

Thus, the present invention provides protease inhibitor synthetic polynucleotides having the sequence of the gene, a nuclear transcript, a cDNA, or complementary  
25 sequences thereof. In preferred embodiments, the nucleic acid library is constructed from *Zea mays*, such as lines B73, PHRE1, A632, BMS-P2#10, and W23, each of which are known and publicly available. In particularly preferred embodiments, the library is constructed from tissue such as root, leaf, or tassel, or embryonic tissue.

The amplification products can be translated using expression systems well known  
30 to those of skill in the art and as discussed, *infra*. The resulting translation products can be confirmed as protease inhibitor polypeptides of the present invention by, for example, assaying for the appropriate inhibition activity or verifying the presence of a linear

epitope which is specific to a protease inhibitor polypeptide using standard immunoassay methods.

Those of ordinary skill will appreciate that primers which selectively amplify, under stringent conditions, the polynucleotides of the present invention (and their complements) can be constructed by reference to the sequences provided herein at SEQ ID NOS: 1,3,5,7,9 and 11. In preferred embodiments, the primers will be constructed to anneal with the first three contiguous nucleotides at their 5' terminal end's to the first codon encoding the carboxy or amino terminal amino acid residue (or the complements thereof) of the polynucleotides of the present invention. Typically, such primers are at least 15 nucleotides in length. The primer length in nucleotides is selected from the group of integers consisting of from at least 15 to 90. Thus, the primers can be at least 15, 18, 20, 25, 30, 40, 50, 60, 70, 80, or 90 nucleotides in length.

The amplification primers may optionally be elongated in the 3' direction with contiguous nucleotide sequences from polynucleotide sequences of SEQ ID NOS: 1,3,5,7,9 and 11, 15,17,19,21, from which they are derived. The number of nucleotides by which the primers can be elongated is selected from the group of integers consisting of from at least 1 to 25. Thus, for example, the primers can be elongated with an additional 1, 5, 10, or 15 nucleotides. Those of skill will recognize that a lengthened primer sequence can be employed to increase specificity of binding (i.e., annealing) to a target sequence.

### *C. Polynucleotides Which Selectively Hybridize to a Polynucleotide of (A) or (B)*

As indicated in (c), *supra*, the present invention provides isolated and/or heterologous nucleic acids comprising protease inhibitor polynucleotides, wherein the polynucleotides selectively hybridize, under selective hybridization conditions, to a protease inhibitor polynucleotide of paragraphs (A) or (B) as discussed, *supra*. Thus, the polynucleotides of this embodiment can be used for isolating, detecting, and/or quantifying nucleic acids comprising the polynucleotides of (A) or (B). Low stringency hybridization conditions are typically, but not exclusively, employed with sequences having relatively small sequence identity. Moderate and high stringency conditions can optionally be employed for sequences of greater identity. Low stringency conditions allow selective hybridization of sequences having about 70% sequence identity.

*D. Polynucleotides Having at Least 60% Sequence Identity with the Polynucleotides of (A), (B) or (C)*

As indicated in (d), *supra*, the present invention provides isolated and/or  
5 heterologous nucleic acids comprising protease inhibitor polynucleotides, wherein the polynucleotides have a specified identity at the nucleotide level to a polynucleotide as disclosed above in paragraphs (A), (B), (C), or (D). The percentage of identity to a reference sequence is at least 60% and, rounded upwards to the nearest integer, can be expressed as an integer selected from the group of integers consisting of from 60 to 99.  
10 Thus, for example, the percentage of identity to a reference sequence can be at least 70%, 75%, 80%, 85%, 90%, or 95%.

Optionally, these polynucleotides encode a first polypeptide which elicits production of antisera comprising antibodies which specifically bind to a second polypeptide encoded by a polynucleotide of (A), (B), or (C). However, the first  
15 polypeptide does not bind to antisera raised against itself when the antisera has been fully immunosorbed with the first polypeptide. Hence, the polynucleotides of this embodiment can be used to generate antibodies for use in, for example, the screening of expression libraries for nucleic acids comprising polynucleotides of (A), (B), or (C), or for purification of, or in immunoassays for, polypeptides encoded by the polynucleotides of  
20 (A), (B), or (C). Further, the polynucleotides of this embodiment embrace those nucleic acid sequences which can be employed for selective hybridization to a polynucleotide encoding a protease inhibitor polypeptide.

*E. Polynucleotides Encoding a Protein Having a Subsequence from a Prototype Polypeptide and Which is Cross-Reactive to the Prototype Polypeptide*

As indicated in (e), *supra*, the present invention provides isolated and/or  
heterologous nucleic acids comprising protease inhibitor polynucleotides, wherein the polynucleotides encode a protein having a subsequence of contiguous amino acids from a prototype protease inhibitor polypeptide. Exemplary prototype protease inhibitor  
30 polypeptides are provided in SEQ ID NOS: 2,4,6,8,10 and 12. The length of contiguous amino acids from the prototype protease inhibitor polypeptide is selected from the group of integers consisting of from at least 10 to the number of amino acids within the

prototype sequence. Thus, for example, the polynucleotide can encode a polypeptide having a subsequence having at least 10, 15, 20, 25, 30, 35, 40, 45, or 50, contiguous amino acids from the prototype polypeptide. Further, the number of such subsequences encoded by a polynucleotide of the instant embodiment can be any integer selected from  
5 the group consisting of from 1 to 20, such as 2, 3, 4, or 5.

The proteins encoded by polynucleotides of this embodiment, when presented as an immunogen, elicit the production of polyclonal antibodies which specifically bind to a prototype protease inhibitor polypeptide such as, but not limited to, a polypeptide encoded by the polynucleotide of (b), *supra*, or exemplary polypeptides of SEQ ID NOS:  
10 2,4,6,8,10 and 12,16,18,20,22,24. Generally, however, a protein encoded by a polynucleotide of this embodiment does not bind to antisera raised against the prototype protease inhibitor polypeptide when the antisera has been fully immunosorbed with the reference protease inhibitor polypeptide. Methods of making and assaying for antibody binding specificity/affinity are well known in the art. Exemplary immunoassay formats  
15 include ELISA, competitive immunoassays, radioimmunoassays, Western blots, indirect immunofluorescent assays and the like.

In a preferred assay method fully immunosorbed and pooled antisera which is elicited to the prototype polypeptide can be used in a competitive binding assay to test the protein. The concentration of the prototype polypeptide required to inhibit 50% of the  
20 binding of the antisera to the prototype polypeptide is determined. If the amount of the protein required to inhibit binding is less than twice the amount of the prototype protein, then the protein is said to specifically bind to the antisera elicited to the immunogen. Accordingly, the proteins embrace allelic variants, conservatively modified variants, and minor recombinant modifications to a prototype protease inhibitor polypeptide.

25 The protease inhibitor polynucleotide optionally encodes a protein having a molecular weight as the unglycosylated protein within 20% of the molecular weight of the truncated or full-length protease inhibitor polypeptides as disclosed herein (e.g., SEQ ID NOS: 2,4,6,8,10 and 12). Preferably, the molecular weight is within 15% of a full length protease inhibitor polypeptide, more preferably within 10% or 5%, and most preferably  
30 within 3%, 2%, or 1% of a full length protease inhibitor polypeptide of the present invention.

Optionally, the protease inhibitor polynucleotides of this embodiment will encode a protein having an inhibitory activity less than or equal to 20%, 30%, 40%, or 50% of the native, endogenous (i.e., non-isolated), full-length protease inhibitor polypeptide.

Determination of protein inhibition can be determined by any number of means well

5 known to those of skill in the art.

*F. Polynucleotides Complementary to the Polynucleotides of (A)-(E)*

As indicated in (f), *supra*, the present invention provides isolated and/or heterologous nucleic acids comprising protease inhibitor polynucleotides, wherein the polynucleotides are complementary to the polynucleotides of paragraphs A-E, above. As those of skill in the art will recognize, complementary sequences base-pair throughout the entirety of their length with the polynucleotides of (A)-(E) (i.e., have 100% sequence identity). Complementary bases associate through hydrogen bonding in double stranded nucleic acids. For example, the following base pairs are complementary: guanine and cytosine; adenine and thymine; and adenine and uracil.

*G. Polynucleotides Which are Subsequences of the Polynucleotides of (A)-(F)*

As indicated in (h), *supra*, the present invention provides isolated and/or heterologous nucleic acids comprising protease inhibitor polynucleotides, wherein the polynucleotide comprises at least 15 contiguous bases from the polynucleotides of (A) through (F) as discussed above. The length of the polynucleotide is given as an integer selected from the group consisting of from at least 15 to the length of the nucleic acid sequence from which the protease inhibitor polynucleotide is a subsequence of. Thus, for example, polynucleotides of the present invention are inclusive of polynucleotides comprising at least 15, 20, 25, 30, 40, 50, 60, 75, or 100 contiguous nucleotides in length from the polynucleotides of (A)-(F). Optionally, the number of such subsequences encoded by a polynucleotide of the instant embodiment can be any integer selected from the group consisting of from 1 to 20, such as 2, 3, 4, or 5.

The subsequences of the present invention can comprise the functional characteristics of the sequence from which it is derived. Alternatively, the subsequences can lack the functional characteristics of the larger sequence from which it is derived. For example, a subsequence from a polynucleotide encoding a polypeptide having at least one

linear epitope in common with a prototype sequence, such as SEQ ID NOS: 2,4,6,8,10 and 12, may encode an epitope in common with the prototype sequence. Alternatively, the subsequence may not encode an epitope in common with the prototype sequence but can be used to isolate the larger sequence by, for example, nucleic acid hybridization with  
5 the sequence from which it's derived.

### **Construction of Protease inhibitor Nucleic Acids**

The isolated and/or heterologous protease inhibitor nucleic acids of the present invention can be made using (a) standard recombinant methods, (b) synthetic techniques,  
10 or combinations thereof. In some embodiments, the protease inhibitor polynucleotides of the present invention will be cloned, amplified, or otherwise constructed from a plant. The preferred plants are barley and *Zea mays*, such as inbred line B73 which is publicly known and available. Particularly preferred is the use of *Zea mays* tissue such as roots, leaves, tassels, seeds or embryonic tissue.

15 Protease inhibitor nucleic acids may conveniently comprise sequences in addition to a protease inhibitor polynucleotide. For example, a multi-cloning site comprising one or more endonuclease restriction sites may be inserted into the nucleic acid to aid in isolation of the polynucleotide. Also, translatable sequences may be inserted to aid in the isolation of the translated protease inhibitor polynucleotide. For example, a hexa-  
20 histidine marker sequence provides a convenient means to purify the proteins of the present invention. In any event, those of skill will appreciate that sequences in addition to a protease inhibitor polynucleotide can be included in a protease inhibitor nucleic acid as desired.

#### ***A. Recombinant Methods for Constructing Protease inhibitor Nucleic Acids***

The isolated and/or heterologous nucleic acid compositions of this invention, such as RNA, cDNA, genomic DNA, or a hybrid thereof, can be obtained from plant biological sources using any number of cloning methodologies known to those of skill in the art.

The isolation of protease inhibitor polynucleotides may be accomplished by a  
30 number of techniques. For instance, oligonucleotide probes based on the sequences disclosed here can be used to identify the desired gene in a cDNA or genomic DNA library. To construct genomic libraries, large segments of genomic DNA are generated by

random fragmentation, e.g. using restriction endonucleases, and are ligated with vector DNA to form concatemers that can be packaged into the appropriate vector. To prepare a cDNA library, mRNA is isolated from the desired organ, such as sclerenchyma and a cDNA library which contains the gene encoding for a protease inhibitor protein (i.e., the protease inhibitor gene) is prepared from the mRNA. Alternatively, cDNA may be prepared from mRNA extracted from other tissues in which protease inhibitor genes or homologs are expressed.

The DNA or genomic library can then be screened using a probe based upon the sequence of a cloned protease inhibitor polynucleotide such as those disclosed herein.

Probes may be used to hybridize with genomic DNA or cDNA sequences to isolate homologous genes in the same or different plant species. Those of skill in the art will appreciate that various degrees of stringency of hybridization can be employed in the assay; and either the hybridization or the wash medium can be stringent. As the conditions for hybridization become more stringent, there must be a greater degree of complementarity between the probe and the target for duplex formation to occur. The degree of stringency can be controlled by temperature, ionic strength, pH and the presence of a partially denaturing solvent such as formamide. For example, the stringency of hybridization is conveniently varied by changing the polarity of the reactant solution through manipulation of the concentration of formamide within the range of 0% to 50%.

Cloning methodologies to accomplish these ends, and sequencing methods to verify the sequence of nucleic acids are well known in the art. Examples of appropriate cloning and sequencing techniques, and instructions sufficient to direct persons of skill through many cloning exercises are found in Sambrook, *et al.*, *Molecular Cloning: A Laboratory Manual*, 2nd Ed., Cold Spring Harbor Laboratory Vols. 1-3 (1989), Methods in Enzymology, Vol. 152: *Guide to Molecular Cloning Techniques*, Berger and Kimmel, Eds., San Diego: Academic Press, Inc. (1987), *Current Protocols in Molecular Biology*, Ausubel, *et al.*, Eds., Greene Publishing and Wiley-Interscience, New York (1987); *Plant Molecular Biology: A Laboratory Manual*, Clark, Ed., Springer-Verlag, Berlin (1997). Product information from manufacturers of biological reagents and experimental equipment also provide information useful in known biological methods. Such manufacturers include the SIGMA chemical company (Saint Louis, MO), R&D systems (Minneapolis, MN), Pharmacia LKB Biotechnology (Piscataway, NJ), CLONTECH

Laboratories, Inc. (Palo Alto, CA), Chem Genes Corp., Aldrich Chemical Company (Milwaukee, WI), Glen Research, Inc., GIBCO BRL Life Technologies, Inc. (Gaithersburg, MD), Fluka Chemica-Biochemika Analytika (Fluka Chemie AG, Buchs, Switzerland), Invitrogen, San Diego, CA, and Applied Biosystems (Foster City, CA), as well as many other commercial sources known to one of skill.

The nucleic acids of interest can also be amplified from nucleic acid samples using amplification techniques. For instance, polymerase chain reaction (PCR) technology can be used to amplify the sequences of protease inhibitor polynucleotides of the present invention and related genes directly from genomic DNA or cDNA libraries. PCR and other *in vitro* amplification methods may also be useful, for example, to clone nucleic acid sequences that code for proteins to be expressed, to make nucleic acids to use as probes for detecting the presence of the desired mRNA in samples, for nucleic acid sequencing, or for other purposes.

The degree of complementarity (sequence identity) required for detectable binding will vary in accordance with the stringency of the hybridization medium and/or wash medium. The degree of complementarity will optimally be 100 percent; however, it should be understood that minor sequence variations in the probes and primers may be compensated for by reducing the stringency of the hybridization and/or wash medium.

Examples of techniques sufficient to direct persons of skill through *in vitro* amplification methods are found in Berger, Sambrook, and Ausubel, as well as Mullis *et al.*, U.S. Patent No. 4,683,202 (1987); *PCR Protocols A Guide to Methods and Applications*, Innis *et al.*, Eds., Academic Press Inc., San Diego, CA (1990); Arnheim & Levinson, *C&EN* pp. 36-47 (October 1, 1990); *The Journal Of NIH Research* 3: 81-94 (1991); Kwok *et al.*, *Proc. Natl. Acad. Sci.* 86: 1173 (1989); Guatelli *et al.*, *Proc. Natl. Acad. Sci.* 87: 1874 (1990); Lomell *et al.*, *J. Clin. Chem.* 35: 1826 (1989); Landegren *et al.*, *Science*, 241: 1077-1080 (1988); Van Brunt, *Biotechnology* 8: 291-294 (1990); Wu and Wallace, *Gene* 4: 560 (1989); and Barringer *et al.*, *Gene* 89: 117 (1990).

#### *B. Synthetic Methods for Constructing Protease inhibitor Nucleic Acids*

The isolated nucleic acids of the present invention can also be prepared by direct chemical synthesis by methods such as the phosphotriester method of Narang *et al.*, *Meth. Enzymol.* 68: 90-99 (1979); the phosphodiester method of Brown *et al.*, *Meth. Enzymol.*



68: 109-151 (1979); the diethylphosphoramidite method of Beaucage *et al.*, Tetra. Lett. 22: 1859-1862 (1981); the solid phase phosphoramidite triester method described by Beaucage and Caruthers, Tetra. Letts. 22(20): 1859-1862 (1981), *e.g.*, using an automated synthesizer, *e.g.*, as described in Needham-VanDevanter *et al.*, Nucleic Acids Res., 12: 6159-6168 (1984); and, the solid support method of U.S. Patent No. 4,458,066. Chemical synthesis generally produces a single stranded oligonucleotide. This may be converted into double stranded DNA by hybridization with a complementary sequence, or by polymerization with a DNA polymerase using the single strand as a template. One of skill will recognize that while chemical synthesis of DNA is limited to sequences of about 100 bases, longer sequences may be obtained by the ligation of shorter sequences.

The isolated nucleic acids of the present invention can also be modified through methods such as site directed mutagenesis, error prone PCR and known to one of skill.

#### 15 **Recombinant Expression Cassettes**

The present invention further provides recombinant expression cassettes comprising a protease inhibitor nucleic acid of the present invention. A nucleic acid sequence coding for the desired protease inhibitor polynucleotide, for example a cDNA or a genomic sequence encoding a full length protease inhibitor protein, can be used to construct a recombinant expression cassette which can be introduced into the desired host cell. A recombinant expression cassette will typically comprise a protease inhibitor polynucleotide operably linked to transcriptional initiation regulatory sequences which will direct the transcription of the protease inhibitor polynucleotide in the intended host cell, such as tissues of a transformed plant.

25 For example, plant expression vectors may include (1) a cloned plant gene under the transcriptional control of 5' and 3' regulatory sequences and (2) a dominant selectable marker. Such plant expression vectors may also contain, if desired, a promoter regulatory region (*e.g.*, one conferring inducible or constitutive, environmentally- or developmentally-regulated, or cell- or tissue-specific/selective expression), a transcription initiation start site, a ribosome binding site, an RNA processing signal, a transcription termination site, and/or

a polyadenylation signal. Highly preferred plant expression cassettes will be designed to include one or more selectable marker genes, such as kanamycin resistance or herbicide tolerance genes.

5           A plant promoter fragment may be employed which will direct expression of the protease inhibitor polynucleotide in all tissues of a regenerated plant. Such promoters are referred to herein as "constitutive" promoters and are active under most environmental conditions and states of development or cell differentiation. Examples of constitutive promoters include the cauliflower mosaic virus (CaMV) 35S transcription initiation  
10   region, the 1'- or 2'- promoter derived from T-DNA of *Agrobacterium tumefaciens*, the ubiquitin 1 promoter, the Smas promoter, the cinnamyl alcohol dehydrogenase promoter (U.S. Patent No. 5,683,439), the *Nos* promoter, the pEmu promoter, the rubisco promoter, the GRP1-8 promoter, and other transcription initiation regions from various plant genes known to those of skill. In a preferred embodiment, the gamma zein promoter of maize  
15   would be used.

          Alternatively, the plant promoter may direct expression of the protease inhibitor polynucleotide in a specific tissue or may be otherwise under more precise environmental or developmental control. Such promoters are referred to here as "inducible" promoters. Environmental conditions that may effect transcription by inducible promoters include  
20   pathogen attack, anaerobic conditions, or the presence of light. Examples of inducible promoters are the *Adh1* promoter which is inducible by hypoxia or cold stress, the *Hsp70* promoter which is inducible by heat stress, and the *PPDK* promoter which is inducible by light.

          Examples of promoters under developmental control include promoters that  
25   initiate transcription only, or preferentially, in certain tissues, such as leaves, roots, fruit, seeds, or flowers. The operation of a promoter may also vary depending on its location in the genome. Thus, an inducible promoter may become fully or partially constitutive in certain locations.

          Both heterologous and non-heterologous (i.e., endogenous) promoters can be  
30   employed to direct expression of the protease inhibitor nucleic acids of the present invention. These promoters can also be used, for example, in recombinant expression cassettes to drive expression of antisense nucleic acids to reduce, increase, or alter

protease inhibitor content and/or composition in a desired tissue. Thus, in some embodiments, the nucleic acid construct will comprise a promoter functional in a plant cell, such as in *Zea mays*, operably linked to an protease inhibitor polynucleotide.

Promoters useful in these embodiments include the endogenous promoters driving protease inhibitor polypeptide expression.

Overproducing plant promoters that may be used in this invention include the promoter of the chlorophyll  $\alpha$ - $\beta$  binding protein, and the promoter of the small sub-unit (ss) of the ribulose-1,5-biphosphate carboxylase from soybean. See e.g. Berry-Lowe, et al., J. Molecular and App. Gen.; Vol. 1; pp. 483-498; (1982); incorporated herein in its entirety by reference. These two promoters are known to be light-induced, in eukaryotic plant cells. See e.g., An Agricultural Perspective, A. Cashmore, Pelham, New York, 1983, pp. 29-38, G. Coruzzi, et al., J. Biol. Chem., Vol. 258; p. 1399 (1983), and P. Dunsmuir, et al., J. Molecular and App. Gen., Vol. 2; p. 285 (1983); all incorporated herein in their entirety by reference.

In some embodiments, isolated nucleic acids which serve as promoter or enhancer elements can be introduced in the appropriate position (generally upstream) of a non-heterologous form of a protease inhibitor polynucleotide of the present invention so as to up or down regulate protease inhibitor polynucleotide expression. For example, endogenous promoters can be altered *in vivo* by mutation, deletion, and/or substitution (see, Kmiec, U.S. Patent 5,565,350; Zarling *et al.*, PCT/US93/03868), or isolated promoters can be introduced into a plant cell in the proper orientation and distance from a protease inhibitor gene so as to control the expression of the gene. Gene expression can thereby be modulated under conditions suitable for plant growth so as to alter protease inhibitor content and/or composition. Thus, the present invention provides compositions, and methods for making, heterologous promoters and/or enhancers operably linked to the native, endogenous (i.e., non-heterologous) forms of the protease inhibitor polynucleotides disclosed herein.

Methods for identifying promoters with a particular expression pattern, in terms of, e.g., tissue type, cell type, stage of development, and/or environmental conditions, are well known in the art. See, e.g., *The Maize Handbook*, Chapters 114-115, Freeling and Walbot, Eds., Springer, New York (1994); *Corn and Corn Improvement*, 3<sup>rd</sup> edition, Chapter 6, Sprague and Dudley, Eds., American Society of Agronomy, Madison,

Wisconsin (1988). A typical step in promoter isolation methods is identification of gene products that are expressed with some degree of specificity in the target tissue. Amongst the range of methodologies are: differential hybridization to cDNA libraries; subtractive hybridization; differential display; differential 2-D gel electrophoresis; DNA probe arrays; and isolation of proteins known to be expressed with some specificity in the target tissue. Such methods are well known to those of skill in the art. Commercially available products for identifying promoters are known in the art such as CloneTech's (Palo Alto, CA) PROMOTERFINDER DNA Walking Kit.

For the protein-based methods, it is helpful to obtain the amino acid sequence for at least a portion of the identified protein, and then to use the protein sequence as the basis for preparing a nucleic acid that can be used as a probe to identify either genomic DNA directly, or preferably, to identify a cDNA clone from a library prepared from the target tissue. Once such a cDNA clone has been identified, that sequence can be used to identify the sequence at the 5' end of the transcript of the indicated gene. For differential hybridization, subtractive hybridization and differential display, the nucleic acid sequence identified as enriched in the target tissue is used to identify the sequence at the 5' end of the transcript of the indicated gene. Once such sequences are identified, starting either from protein sequences or nucleic acid sequences, any of these sequences identified as being from the gene transcript can be used to screen a genomic library prepared from the target organism. Methods for identifying and confirming the transcriptional start site are well known in the art.

In the process of isolating promoters expressed under particular environmental conditions or stresses, or in specific tissues, or at particular developmental stages, a number of genes are identified that are expressed under the desired circumstances, in the desired tissue, or at the desired stage. Further analysis will reveal expression of each particular gene in one or more other tissues of the plant. One can identify a promoter with activity in the desired tissue or condition but that do not have activity in any other common tissue.

To identify the promoter sequence, the 5' portions of the clones described here are analyzed for sequences characteristic of promoter sequences. For instance, promoter sequence elements include the TATA box consensus sequence (TATAAT), which is usually an AT-rich stretch of 5-10 bp located approximately 20 to 40 base pairs upstream

of the transcription start site. Identification of the TATA box is well known in the art. For example, one way to predict the location of this element is to identify the transcription start site using standard RNA-mapping techniques such as primer extension, S1 analysis, and/or RNase protection. To confirm the presence of the AT-rich sequence, a structure-function analysis can be performed involving mutagenesis of the putative region and quantification of the mutation's effect on expression of a linked downstream reporter gene. See, e.g., *The Maize Handbook*, Chapter 114, Freeling and Walbot, Eds., Springer, New York, (1994).

In plants, further upstream from the TATA box, at positions -80 to -100, there is typically a promoter element (i.e., the CAAT box) with a series of adenines surrounding the trinucleotide G (or T) N G. J. Messing *et al.*, in *Genetic Engineering in Plants*, Kosage, Meredith and Hollaender, Eds., pp. 221-227 1983. In maize, there is no well conserved CAAT box but there are several short, conserved protein-binding motifs upstream of the TATA box. These include motifs for the trans-acting transcription factors involved in light regulation, anaerobic induction, hormonal regulation, or anthocyanin biosynthesis, as appropriate for each gene.

Once promoter and/or gene sequences are known, a region of suitable size is selected from the genomic DNA that is 5' to the transcriptional start, or the translational start site, and such sequences are then linked to a coding sequence. If the transcriptional start site is used as the point of fusion, any of a number of possible 5' untranslated regions can be used in between the transcriptional start site and the partial coding sequence. If the translational start site at the 3' end of the specific promoter is used, then it is linked directly to the methionine start codon of a coding sequence.

If polypeptide expression is desired, it is generally desirable to include a polyadenylation region at the 3'-end of the protease inhibitor polynucleotide coding region. The polyadenylation region can be derived from the natural gene, from a variety of other plant genes, or from T-DNA. The 3' end sequence to be added can be derived from, for example, the nopaline synthase or octopine synthase genes, or alternatively from another plant gene, or less preferably from any other eukaryotic gene.

An intron sequence can be added to the 5' untranslated region or the coding sequence of the partial coding sequence to increase the amount of the mature message that accumulates in the cytosol. Inclusion of a spliceable intron in the transcription unit in

both plant and animal expression constructs has been shown to increase gene expression at both the mRNA and protein levels up to 1000-fold. Buchman and Berg, Mol. Cell Biol. 8: 4395-4405 (1988); Callis *et al.*, Genes Dev. 1: 1183-1200 (1987). Such intron enhancement of gene expression is typically greatest when placed near the 5' end of the transcription unit. Use of maize introns Adh1-S intron 1, 2, and 6, the Bronze-1 intron are known in the art. See generally, *The Maize Handbook*, Chapter 116, Freeling and Walbot, Eds., Springer, New York (1994).

The vector comprising the sequences from a protease inhibitor nucleic acid will typically comprise a marker gene which confers a selectable phenotype on plant cells. Usually, the selectable marker gene will encode antibiotic resistance, with suitable genes including genes coding for resistance to the antibiotic spectinomycin (e.g., the *aada* gene), the streptomycin phosphotransferase (SPT) gene coding for streptomycin resistance, the neomycin phosphotransferase (NPTII) gene encoding kanamycin or geneticin resistance, the hygromycin phosphotransferase (HPT) gene coding for hygromycin resistance, genes coding for resistance to herbicides which act to inhibit the action of acetolactate synthase (ALS), in particular the sulfonylurea-type herbicides (e.g., the acetolactate synthase (ALS) gene containing mutations leading to such resistance in particular the S4 and/or Hra mutations), genes coding for resistance to herbicides which act to inhibit action of glutamine synthase, such as phosphinothricin or basta (e.g., the *bar* gene), or other such genes known in the art. The *bar* gene encodes resistance to the herbicide basta, the *nptII* gene encodes resistance to the antibiotics kanamycin and geneticin, and the ALS gene encodes resistance to the herbicide chlorsulfuron.

Typical vectors useful for expression of genes in higher plants are well known in the art and include vectors derived from the tumor-inducing (Ti) plasmid of *Agrobacterium tumefaciens* described by Rogers *et al.*, Meth. In Enzymol., 153:253-277 (1987). These vectors are plant integrating vectors in that on transformation, the vectors integrate a portion of vector DNA into the genome of the host plant. Exemplary *A. tumefaciens* vectors useful herein are plasmids pKYLX6 and pKYLX7 of Schardl *et al.*, Gene, 61:1-11 (1987) and Berger *et al.*, Proc. Natl. Acad. Sci. U.S.A., 86:8402-8406 (1989). Another useful vector herein is plasmid pBI101.2 that is available from Clontech Laboratories, Inc. (Palo Alto, CA).

The protease inhibitor polynucleotide of the present invention can be expressed in either sense or anti-sense orientation as desired. It will be appreciated that control of gene expression in either sense or anti-sense orientation can have a direct impact on the observable plant characteristics. Antisense technology can be conveniently used to  
5 reduce gene expression in plants. To accomplish this, a nucleic acid segment from the desired gene is cloned and operably linked to a promoter such that the anti-sense strand of RNA will be transcribed. The construct is then transformed into plants and the antisense strand of RNA is produced. In plant cells, it has been shown that antisense RNA inhibits gene expression by preventing the accumulation of mRNA which encodes the enzyme of  
10 interest, see, e.g., Sheehy *et al.*, Proc. Nat'l. Acad. Sci. (USA) 85: 8805-8809 (1988); and Hiatt *et al.*, U.S. Patent No. 4,801,340.

Another method of suppression is sense suppression. Introduction of nucleic acid configured in the sense orientation has been shown to be an effective means by which to block the transcription of target genes. For an example of the use of this method to  
15 modulate expression of endogenous genes see, Napoli *et al.*, The Plant Cell 2: 279-289 (1990) and U.S. Patent No. 5,034,323.

Catalytic RNA molecules or ribozymes can also be used to inhibit expression of plant genes. It is possible to design ribozymes that specifically pair with virtually any target RNA and cleave the phosphodiester backbone at a specific location, thereby  
20 functionally inactivating the target RNA. In carrying out this cleavage, the ribozyme is not itself altered, and is thus capable of recycling and cleaving other molecules, making it a true enzyme. The inclusion of ribozyme sequences within antisense RNAs confers RNA-cleaving activity upon them, thereby increasing the activity of the constructs. The design and use of target RNA-specific ribozymes is described in Haseloff *et al.*, Nature  
25 334: 585-591 (1988).

### **Protease inhibitor Proteins**

The isolated protease inhibitor proteins of the present invention comprise a protease inhibitor polypeptide having at least 10 amino acids encoded by any one of the  
30 protease inhibitor polynucleotides as discussed more fully, *supra*, or polypeptides which are conservatively modified variants thereof. Exemplary protease inhibitor polypeptide sequences are provided in SEQ ID NOS: 2,4,6,8,10 and 12. The protease inhibitor

proteins of the present invention or variants thereof can comprise any number of contiguous amino acid residues from a protease inhibitor protein, wherein that number is selected from the group of integers consisting of from 10 to the number of residues in a full-length protease inhibitor polypeptide. Optionally, this subsequence of contiguous amino acids is at least 15, 20, 25, 30, 35, or 40 amino acids in length, often at least 50, 60, 70, 80, or 90 amino acids in length. Further, the number of such subsequences can be any integer selected from the group consisting of from 1 to 20, such as 2, 3, 4, or 5.

As those of skill will appreciate, the present invention includes protease inhibitor polypeptides with less inhibitory activity. Less inhibitory protease inhibitor polypeptides have an inhibitory activity at least 20%, 30%, or 40%, and preferably at least 50% or 60%, below that of the native (non-synthetic), endogenous protease inhibitor polypeptide.

Generally, the protease inhibitor proteins of the present invention will, when presented as an immunogen, elicit production of an antibody specifically reactive to a protease inhibitor polypeptide encoded by the protease inhibitor polynucleotide as described, *supra*. Exemplary polypeptides include those which are full-length, such as those disclosed in SEQ ID NOS: 2,4,6,8,10 and 12. Further, the protease inhibitor proteins will not bind to antisera raised against a protease inhibitor polypeptide (e.g., SEQ ID NOS: 2,4,6,8,10 and 12) which has been fully immunosorbed with the same protease inhibitor polypeptide. Immunoassays for determining binding are well known to those of skill in the art. A preferred immunoassay is a competitive immunoassay as discussed, *infra*. Thus, the protease inhibitor proteins can be employed as immunogens for constructing antibodies immunoreactive to a protease inhibitor protein for such exemplary utilities as immunoassays or protein purification techniques.

## **Expression of Proteins in Host Cells**

Using the nucleic acids of the present invention, one may express a protease inhibitor protein in a recombinantly engineered cell such as bacteria, yeast, insect, mammalian, or preferably plant cells. The cells produce the protein in a non-natural condition (e.g., in quantity, composition, location, and/or time), because they have been genetically altered through human intervention to do so.

It is expected that those of skill in the art are knowledgeable in the numerous expression systems available for expression of nucleic acids encoding protease inhibitor



proteins. No attempt to describe in detail the various methods known for the expression of proteins in prokaryotes or eukaryotes will be made.

In brief summary, the expression of isolated nucleic acids encoding protease inhibitor proteins will typically be achieved by operably linking, for example, the DNA or cDNA to a promoter (which is either constitutive or inducible), followed by incorporation into an expression vector. The vectors can be suitable for replication and integration in either prokaryotes or eukaryotes. Typical expression vectors contain transcription and translation terminators, initiation sequences, and promoters useful for regulation of the expression of the DNA encoding the protease inhibitor protein. To obtain high level expression of a cloned gene, it is desirable to construct expression vectors which contain, at the minimum, a strong promoter to direct transcription, a ribosome binding site for translational initiation, and a transcription/translation terminator. One of skill would recognize that modifications can be made to an protease inhibitor protein without diminishing its biological activity. Some modifications may be made to facilitate the cloning, expression, or incorporation of the targeting molecule into a fusion protein. Such modifications are well known to those of skill in the art and include, for example, a methionine added at the amino terminus to provide an initiation site, or additional amino acids (*e.g.*, poly His) placed on either terminus to create conveniently located restriction sites or termination codons or purification sequences.

#### *A. Expression in Prokaryotes*

Prokaryotic cells may be used as hosts for expression. Prokaryotes most frequently are represented by various strains of *E. coli*; however, other microbial strains may also be used. Commonly used prokaryotic control sequences which are defined herein to include promoters for transcription initiation, optionally with an operator, along with ribosome binding site sequences, include such commonly used promoters as the beta lactamase (penicillinase) and lactose (lac) promoter systems (Chang et al., Nature 198:1056 (1977)), the tryptophan (trp) promoter system (Goeddel et al., Nucleic Acids Res. 8:4057 (1980)) and the lambda derived P<sub>L</sub> promoter and N-gene ribosome binding site (Shimatake *et al.*, Nature 292:128 (1981)). The inclusion of selection markers in DNA vectors transfected in *E. coli* is also useful. Examples of such markers include genes specifying resistance to ampicillin, tetracycline, or chloramphenicol.

The vector is selected to allow introduction into the appropriate host cell.

Bacterial vectors are typically of plasmid or phage origin. Appropriate bacterial cells are infected with phage vector particles or transfected with naked phage vector DNA. If a plasmid vector is used, the bacterial cells are transfected with the plasmid vector DNA.

5 Expression systems for expressing protease inhibitor proteins are available using *Bacillus* *sp.* and *Salmonella* (Palva, *et al.*, Gene 22: 229-235 (1983); Mosbach, *et al.*, Nature 302: 543-545 (1983)).

#### *B. Expression in Eukaryotes*

10 A variety of eukaryotic expression systems such as yeast, insect cell lines, plant and mammalian cells, are known to those of skill in the art. As explained briefly below, protease inhibitor proteins of the present invention may be expressed in these eukaryotic systems. In some embodiments, transformed/transfected plant cells, as discussed *infra*, are employed as expression systems for production of the proteins of the instant  
15 invention.

Synthesis of heterologous proteins in yeast is well known. Sherman, F., *et al.*, *Methods in Yeast Genetics*, Cold Spring Harbor Laboratory (1982) is a well recognized work describing the various methods available to produce the protein in yeast. Suitable vectors usually have expression control sequences, such as promoters, including 3-  
20 phosphoglycerate kinase or other glycolytic enzymes, and an origin of replication, termination sequences and the like as desired. For instance, suitable vectors are described in the literature (Botstein, *et al.*, Gene 8: 17-24 (1979); Broach, *et al.*, Gene 8: 121-133 (1979)).

Protease inhibitor proteins, once expressed, can be isolated from yeast by lysing  
25 the cells and applying standard protein isolation techniques to the lysates. The monitoring of the purification process can be accomplished by using Western blot techniques or radioimmunoassay of other standard immunoassay techniques.

The sequences encoding protease inhibitor proteins can also be ligated to various expression vectors for use in transfecting cell cultures of, for instance, mammalian, insect,  
30 or plant origin. Illustrative of cell cultures useful for the production of the peptides are mammalian cells. Mammalian cell systems often will be in the form of monolayers of cells although mammalian cell suspensions may also be used. A number of suitable host

cell lines capable of expressing intact proteins have been developed in the art, and include the HEK293, BHK21, and CHO cell lines. Expression vectors for these cells can include expression control sequences, such as an origin of replication, a promoter (*e.g.*, the CMV promoter, a HSV *tk* promoter or *pgk* (phosphoglycerate kinase) promoter), an enhancer (Queen *et al.*, Immunol. Rev. 89: 49 (1986)), and necessary processing information sites, such as ribosome binding sites, RNA splice sites, polyadenylation sites (*e.g.*, an SV40 large T Ag poly A addition site), and transcriptional terminator sequences. Other animal cells useful for production of protease inhibitor proteins are available, for instance, from the American Type Culture Collection Catalogue of Cell Lines and Hybridomas (7th edition, 1992).

Appropriate vectors for expressing protease inhibitor proteins in insect cells are usually derived from the SF9 baculovirus. Suitable insect cell lines include mosquito larvae, silkworm, armyworm, moth and *Drosophila* cell lines such as a Schneider cell line (See Schneider, J. Embryol. Exp. Morphol. 27: 353-365 (1987).

As with yeast, when higher animal or plant host cells are employed, polyadenylation or transcription terminator sequences are typically incorporated into the vector. An example of a terminator sequence is the polyadenylation sequence from the bovine growth hormone gene. Sequences for accurate splicing of the transcript may also be included. An example of a splicing sequence is the VP1 intron from SV40 (Sprague, *et al.*, J. Virol. 45: 773-781 (1983)). Additionally, gene sequences to control replication in the host cell may be incorporated into the vector such as those found in bovine papilloma virus type-vectors. Saveria-Campo, M., Bovine Papilloma Virus DNA a Eukaryotic Cloning Vector in *DNA Cloning Vol. II a Practical Approach*, D.M. Glover, Ed., IRL Press, Arlington, Virginia pp. 213-238 (1985).

### **Transfection/Transformation of Cells**

The method of transformation/transfection is not critical to the instant invention; various methods of transformation or transfection are currently available. As newer methods are available to transform crops or other host cells they may be directly applied. Accordingly, a wide variety of methods have been developed to insert a DNA sequence into the genome of a host cell to obtain the transcription and/or translation of the sequence

to effect phenotypic changes in the organism. Thus, any method which provides for efficient transformation/transfection may be employed.

#### A. Plant Transformation

5           A DNA sequence coding for the desired protease inhibitor polynucleotide, for example a cDNA or a genomic sequence encoding a full length protein, will be used to construct a recombinant expression cassette which can be introduced into the desired plant.

Isolated nucleic acids of the present invention can be introduced into plants  
10 according to techniques known in the art. Generally, recombinant expression cassettes as described above and suitable for transformation of plant cells are prepared. Techniques for transforming a wide variety of higher plant species are well known and described in the technical, scientific, and patent literature. See, for example, Weising *et al.*, Ann. Rev. Genet. 22: 421-477 (1988). For example, the DNA construct may be introduced directly  
15 into the genomic DNA of the plant cell using techniques such as electroporation, PEG poration, particle bombardment, silicon fiber delivery, or microinjection of plant cell protoplasts or embryogenic callus. Alternatively, the DNA constructs may be combined with suitable T-DNA flanking regions and introduced into a conventional *Agrobacterium tumefaciens* host vector. The virulence functions of the *Agrobacterium tumefaciens* host  
20 will direct the insertion of the construct and adjacent marker into the plant cell DNA when the cell is infected by the bacteria.

The introduction of DNA constructs using polyethylene glycol precipitation is described in Paszkowski *et al.*, Embo J. 3: 2717-2722 (1984). Electroporation techniques are described in Fromm *et al.*, Proc. Natl. Acad. Sci. 82: 5824 (1985). Ballistic  
25 transformation techniques are described in Klein *et al.*, Nature 327: 70-73 (1987). *Agrobacterium tumefaciens*-mediated transformation techniques are well described in the scientific literature. See, for example Horsch *et al.*, Science 233: 496-498 (1984), and Fraley *et al.*, Proc. Natl. Acad. Sci. 80: 4803 (1983). Although *Agrobacterium* is useful primarily in dicots, certain monocots can be transformed by *Agrobacterium*. For instance,  
30 *Agrobacterium* transformation of maize is described in U.S. Patent No. 5,550,318.

Other methods of transfection or transformation include (1) *Agrobacterium rhizogenes*-mediated transformation (see, e.g., Lichtenstein and Fuller In: Genetic

Engineering, vol. 6, PWJ Rigby, Ed., London, Academic Press, 1987; and Lichtenstein, C. P., and Draper, J., In: DNA Cloning, Vol. II, D. M. Glover, Ed., Oxford, IRI Press, 1985), Application PCT/US87/02512 (WO 88/02405 published Apr. 7, 1988) describes the use of *A. rhizogenes* strain A4 and its Ri plasmid along with *A. tumefaciens* vectors  
 5 pARC8 or pARC16 (2) liposome-mediated DNA uptake (see, e.g., Freeman *et al.*, Plant Cell Physiol. 25: 1353, 1984), (3) the vortexing method (see, e.g., Kindle, *Proc. Natl. Acad. Sci.*, USA 87: 1228, (1990).

DNA can also be introduced into plants by direct DNA transfer into pollen as described by Zhou *et al.*, Methods in Enzymology, 101:433 (1983); D. Hess, Intern  
 10 Rev. Cytol., 107:367 (1987); Luo *et al.*, Plant Mol. Biol. Reporter, 6:165 (1988). Expression of polypeptide coding genes can be obtained by injection of the DNA into reproductive organs of a plant as described by Pena *et al.*, Nature, 325.:274 (1987). DNA can also be injected directly into the cells of immature embryos and the rehydration of desiccated embryos as described by Neuhaus *et al.*,  
 15 *Theor. Appl. Genet.*, 75:30 (1987); and Benbrook *et al.*, in Proceedings Bio Expo 1986, Butterworth, Stoneham, Mass., pp. 27-54 (1986). A variety of plant viruses that can be employed as vectors are known in the art and include cauliflower mosaic virus (CaMV), geminivirus, brome mosaic virus, and tobacco mosaic virus.

## 20 *B. Transfection of Prokaryotes, Lower Eukaryotes, and Animal Cells*

Animal and lower eukaryotic (e.g., yeast) host cells are competent or rendered competent for transfection by various means. There are several well-known methods of introducing DNA into animal cells. These include: calcium phosphate precipitation, fusion of the recipient cells with bacterial protoplasts containing the DNA, treatment of  
 25 the recipient cells with liposomes containing the DNA, DEAE dextran, electroporation, biolistics, and micro-injection of the DNA directly into the cells. The transfected cells are cultured by means well known in the art. Kuchler, R.J., *Biochemical Methods in Cell Culture and Virology*, Dowden, Hutchinson and Ross, Inc. (1977).

## 30 Synthesis of Proteins

Protease inhibitor proteins of the present invention can be constructed using non-cellular synthetic methods. Solid phase synthesis of protease inhibitor proteins of less

than about 50 amino acids in length may be accomplished by attaching the C-terminal amino acid of the sequence to an insoluble support followed by sequential addition of the remaining amino acids in the sequence. Techniques for solid phase synthesis are described by Barany and Merrifield, *Solid-Phase Peptide Synthesis*, pp. 3-284 in *The Peptides: Analysis, Synthesis, Biology. Vol. 2: Special Methods in Peptide Synthesis, Part A.*; Merrifield, *et al.*, J. Am. Chem. Soc. 85: 2149-2156 (1963), and *Stewart et al., Solid Phase Peptide Synthesis, 2nd ed.*, Pierce Chem. Co., Rockford, Ill. (1984). Also, the compounds can be synthesized on an applied Biosystems model 431a peptide synthesizer using fastmoc™ chemistry involving hbtu [2-(1h-benzotriazol-1-yl)-1,1,3,3-tetramethyluronium hexafluorophosphate, as published by Rao, *et al.*, Int. J. Pep. Prot. Res.; Vol. 40; pp. 508-515; (1992); incorporated herein in its entirety by reference. Peptides can be cleaved following standard protocols and purified by reverse phase chromatography using standard methods. The amino acid sequence of each peptide can be confirmed by automated edman degradation on an applied biosystems 477a protein sequencer/120a pth analyzer. Protease inhibitor proteins of greater length may be synthesized by condensation of the amino and carboxy termini of shorter fragments. Methods of forming peptide bonds by activation of a carboxy terminal end (e.g., by the use of the coupling reagent N,N'-dicyclohexylcarbodiimide)) is known to those of skill.

## **Purification of Proteins**

The protease inhibitor proteins of the present invention may be purified by standard techniques well known to those of skill in the art. Recombinantly produced protease inhibitor proteins can be directly expressed or expressed as a fusion protein. The recombinant protease inhibitor protein is purified by a combination of cell lysis (e.g., sonication, French press) and affinity chromatography. For fusion products, subsequent digestion of the fusion protein with an appropriate proteolytic enzyme releases the desired recombinant protease inhibitor protein.

The protease inhibitor proteins of this invention, recombinant or synthetic, may be purified to substantial purity by standard techniques well known in the art, including selective precipitation with such substances as ammonium sulfate, column chromatography, immunopurification methods, and others. *See, for instance, R. Scopes, Protein Purification: Principles and Practice*, Springer-Verlag: New York (1982);

Deutscher, *Guide to Protein Purification*, Academic Press (1990). For example, antibodies may be raised to the protease inhibitor proteins as described herein. Purification from *E. coli* can be achieved following procedures described in U.S. Patent No. 4,511,503. The protein may then be isolated from cells expressing the protease inhibitor protein and further purified by standard protein chemistry techniques as described herein. Detection of the expressed protein is achieved by methods known in the art and include, for example, radioimmunoassays, Western blotting techniques, protease inhibition assays, or immunoprecipitation.

## 10 **Transgenic Plant Regeneration**

Transformed plant cells which are derived by any of the above transformation techniques can be cultured to regenerate a whole plant which possesses the transformed genotype and thus the desired protease inhibitor content and/or composition phenotype. Such regeneration techniques often rely on manipulation of certain phytohormones in a tissue culture growth medium, typically relying on a biocide and/or herbicide marker which has been introduced together with the protease inhibitor polynucleotide.

Plants cells transformed with a plant expression vector can be regenerated, e.g., from single cells, callus tissue or leaf discs according to standard plant tissue culture techniques. It is well known in the art that various cells, tissues, and organs from almost any plant can be successfully cultured to regenerate an entire plant. Plant regeneration from cultured protoplasts is described in Evans *et al.*, *Protoplasts Isolation and Culture, Handbook of Plant Cell Culture*, Macmillan Publishing Company, New York, pp. 124-176 (1983); and Binding, *Regeneration of Plants, Plant Protoplasts*, CRC Press, Boca Raton, pp. 21-73 (1985).

The regeneration of plants containing the foreign gene introduced by *Agrobacterium* from leaf explants can be achieved as described by Horsch *et al.*, Science, 227:1229-1231 (1985). In this procedure, transformants are grown in the presence of a selection agent and in a medium that induces the regeneration of shoots in the plant species being transformed as described by Fraley *et al.*, Proc. Natl. Acad. Sci. U.S.A., 80:4803 (1983). This procedure typically produces shoots within two to four weeks and these transformant shoots are then transferred to an appropriate root-inducing medium containing the selective

agent and an antibiotic to prevent bacterial growth. Transgenic plants of the present invention may be fertile or sterile.

Regeneration can also be obtained from plant callus, explants, organs, or parts thereof. Such regeneration techniques are described generally in Klee *et al.*, Ann. Rev. of Plant Phys. 38: 467-486 (1987). The regeneration of plants from either single plant protoplasts or various explants is well known in the art. See, for example, Methods for Plant Molecular Biology, A. Weissbach and H. Weissbach, eds., Academic Press, Inc., San Diego, Calif. (1988). This regeneration and growth process includes the steps of selection of transformant cells and shoots, rooting the transformant shoots and growth of the plantlets in soil. For maize cell culture and regeneration see generally, *The Maize Handbook*, Freeling and Walbot, Eds., Springer, New York (1994); *Corn and Corn Improvement*, 3<sup>rd</sup> edition, Sprague and Dudley Eds., American Society of Agronomy, Madison, Wisconsin (1988).

One of skill will recognize that after the recombinant expression cassette is stably incorporated in transgenic plants and confirmed to be operable, it can be introduced into other plants by sexual crossing. Any of a number of standard breeding techniques can be used, depending upon the species to be crossed.

In vegetatively propagated crops, mature transgenic plants can be propagated by the taking of cuttings or by tissue culture techniques to produce multiple identical plants. Selection of desirable transgenics is made and new varieties are obtained and propagated vegetatively for commercial use. In seed propagated crops, mature transgenic plants can be self crossed to produce a homozygous inbred plant. The inbred plant produces seed containing the newly introduced heterologous nucleic acid. These seeds can be grown to produce plants that would produce the selected phenotype, (e.g., altered protease inhibitor content or composition).

Parts obtained from the regenerated plant, such as flowers, seeds, leaves, branches, fruit, and the like are included in the invention, provided that these parts comprise cells comprising the isolated nucleic acid of the present invention. Progeny and variants, and mutants of the regenerated plants are also included within the scope of the invention, provided that these parts comprise the introduced nucleic acid sequences.

Transgenic plants expressing the selectable marker can be screened for



transmission of the protease inhibitor nucleic acid of the present invention by, for example, standard immunoblot and DNA detection techniques. Transgenic lines are also typically evaluated on levels of expression of the heterologous nucleic acid. Expression at the RNA level can be determined initially to identify and quantitate expression-positive plants. Standard techniques for RNA analysis can be employed and include PCR amplification assays using oligonucleotide primers designed to amplify only the heterologous RNA templates and solution hybridization assays using heterologous nucleic acid-specific probes. The RNA-positive plants can then analyzed for protein expression by Western immunoblot analysis using the protease inhibitor specific antibodies of the present invention. In addition, *in situ* hybridization and immunocytochemistry according to standard protocols can be done using heterologous nucleic acid specific polynucleotide probes and antibodies, respectively, to localize sites of expression within transgenic tissue. Generally, a number of transgenic lines are usually screened for the incorporated nucleic acid to identify and select plants with the most appropriate expression profiles.

A preferred embodiment is a transgenic plant that is homozygous for the added heterologous nucleic acid; i.e., a transgenic plant that contains two added nucleic acid sequences, one gene at the same locus on each chromosome of a chromosome pair. A homozygous transgenic plant can be obtained by sexually mating (selfing) a heterozygous transgenic plant that contains a single added heterologous nucleic acid, germinating some of the seed produced and analyzing the resulting plants produced for altered activity relative to a control plant (i.e., native, non-transgenic). Back-crossing to a parental plant and out-crossing with a non- transgenic plant are also contemplated.

#### Protein structure and amino acid substitution

It can be difficult to predict the ultimate effect of substitution on the tertiary structure and folding of the protein. Both tertiary structure and folding are critical to the stability and adequate expression of the protein *in vivo*. It is critical to undertake analysis and functional modeling of the wild type compound to determine whether substitutions can be made without disrupting biological activity.

The biological activity of a protein is dictated by its three dimensional structure which is intrinsically related to the folding of the protein. The folding of a protein into its functional domains is a direct consequence of the primary amino acid sequence. While it

is true that many proteins tolerate amino acid changes without affecting the folding or function of the protein, there is no a priori method of predicting which amino acid may be substituted or deleted without affecting the folding pathway. Each protein is unique and the folding process is necessarily an experimental determination. As has been concluded

5 by Zabin et al., ("Approaches to Predicting Effects of Single Amino Acid Substitutions on the Function of a Protein"; Biochemistry; Vol. 30; pp. 6230-6240; 1991), neither the frequency of exchange of amino acids between homologous proteins nor any other measure of the properties of the amino acids are particularly useful by themselves in predicting whether a protein with an amino acid substitution will be functional. The

10 scientific literature is replete with examples where seemingly conservative substitutions have resulted in major perturbations of structure and activity and vice versa, see e.g.; Summers, et al., "A Conservative Amino Acid Substitution, Arginine for Lysine, Abolishes Export of a Hybrid Protein in E. Coli," J. Biol. Chem., Vol. 264, pp. 20082-20088, (1989); Ringe, D., "The Sheep in Wolf's Clothing" Nature, Vol. 339, pp. 658-659,

15 (1989); Hirabayashi et al., "Effect of Amino Acid Substitution by Site-directed Mutagenesis on the Carbohydrate Recognition and Stability of Human 14-kDa  $\beta$ -galactoside-binding Lectin," J. Biol. Chem., Vol. 266, pp. 23648-23653, (1991); and van Eijsden, et al., "Mutational Analysis of Pea Lectin: Substitution of Asn125 for Asp in the Monosachharide-binding Site Eliminates Mannose/Glucose -binding Activity," Plant

20 Mol. Biol., Vol. 20, pp. 1049-1058 (1992); all incorporated herein in their entirety by reference.

The 3D structure of many proteins, including enzymes and protein inhibitors such as the barley chymotrypsin inhibitor has been solved. The three dimensional structure of a truncated fragment of CI-2 (with 65 residues) that is missing the N-terminal 18 residues

25 has been determined by x-ray crystallography as well as by NMR spectroscopy (McPhalen, et al., Biochemistry; Vol. 26; pp. 261-269; (1987); and Clore, et al., Protein Eng.; Vol. 1, pp. 313-318; (1987)). In the wild type CI-2 the first 18 residues do not assume any ordered conformation and also do not contribute to the structural integrity of the molecule (see e.g. Kjaer, et al., Carlsberg Res. Commun.; Vol. 53; pp. 327-354;

30 (1987); incorporated herein in its entirety by reference), This polypeptide is found in the endosperm of grain and is isolated as an 83 residue protein with no disulfide bridges. See e.g. Jonassen, I., Carlsberg Res. Commun.; Vol. 45; pp. 47-48; (1980); and Svendsen, I.,

et al., Carlsberg Res. Commun.; Vol. 45; pp. 79-85; (1980). The 3D structure of CI-2 has been determined. See McPhalen, et al., 1987; incorporated herein in its entirety by reference. CI-2 is predominantly a  $\beta$ -sheet protein, devoid of disulfide bonds and containing a wide loop of approximately 18 residues (residue 53-70 in the CI-2 molecule) in the extended conformation. This is the reactive site loop that contains a methionine residue at position 59 which confers the property of chymotrypsin inhibition. A constrained peptide containing these residues has been synthesized and shown to retain full chymotrypsin inhibitory activity. See Leatherbarrow, et al., Biochem., Vol. 30, pp. 10717-10721 (1991). In the absence of any disulfide bonds, the integrity of the reactive site loop is maintained by strong hydrogen bond interactions between Glu60  $\rightarrow$  Arg65 and Thr58  $\rightarrow$  Arg67. Mutants of CI-2 in which Thr58 and Glu60 have been replaced with Ala are not only less stable proteins but also have little or no protease inhibitory activity. See Jackson, et al., Biochem., Vol. 33, pp. 13880-13887 (1994); and Jandu, et al., Biochem., Vol. 33, pp. 6264-6269 (1990). These studies have demonstrated that the reactive site loop is a key structural feature essential for the function of protease inhibition.

### **Molecular Markers**

The present invention provides a method of genotyping a plant comprising a protease inhibitor polynucleotide. Preferably, the plant is a monocot, such as maize or sorghum. Genotyping provides a means of distinguishing homologs of a chromosome pair and can be used to differentiate segregants in a plant population.

Molecular marker methods can be used for phylogenetic studies, characterizing genetic relationships among crop varieties, identifying crosses or somatic hybrids, localizing chromosomal segments affecting monogenic traits, map based cloning, and the study of quantitative inheritance. See, e.g., *Plant Molecular Biology: A Laboratory Manual*, Chapter 7, Clark, Ed., Springer-Verlag, Berlin (1997). For molecular marker methods, see generally, *The DNA Revolution* by Andrew H. Paterson 1996 (Chapter 2) in: *Genome Mapping in Plants* (ed. Andrew H. Paterson) by Academic Press/R. G. Landis Company, Austin, Texas, pp.7-21.

The particular method of genotyping in the present invention may employ any number of molecular marker analytic techniques such as, but not limited to, restriction fragment length polymorphisms (RFLPs). RFLPs are the product of allelic differences between DNA restriction fragments caused by nucleotide sequence variability.

5 As is well known to those of skill in the art, RFLPs are typically detected by extraction of genomic DNA and digestion with a restriction enzyme. Generally, the resulting fragments are separated according to size and hybridized with a probe; single copy probes are preferred. Restriction fragments from homologous chromosomes are revealed.

Differences in fragment size among alleles represent an RFLP. Thus, the present  
10 invention further provides a means to follow segregation of protease inhibitor genes of the present invention as well as chromosomal sequences genetically linked to protease inhibitor genes using such techniques as RFLP analysis. Linked chromosomal sequences are within 50 centiMorgans (cM), often within 40 or 30 cM, preferably within 20 or 10 cM, more preferably within 5, 3, 2, or 1 cM of a protease inhibitor gene of the present  
15 invention.

In the present invention, the nucleic acid probes employed for molecular marker mapping of plant nuclear genomes selectively hybridize, under selective hybridization conditions, to a gene encoding a protease inhibitor polynucleotide. In preferred embodiments, the probes are selected from protease inhibitor polynucleotides.

20 Typically, these probes are cDNA probes or *Pst I* genomic clones. The length of protease inhibitor probes are discussed in greater detail, *supra*, but are typically at least 15 bases in length, more preferably at least 20, 25, 30, 35, 40, or 50 bases in length. Generally, however, the probes are less than about 1 kilobase in length. Preferably, the probes are single copy probes that hybridize to a unique locus in a haploid chromosome  
25 complement. Some exemplary restriction enzymes employed in RFLP mapping are EcoRI, EcoRV, and SstI. As used herein the term "restriction enzyme" includes reference to a composition that recognizes and, alone or in conjunction with another composition, cleaves at a specific nucleotide sequence.

The method of detecting an RFLP comprises the steps of (a) digesting  
30 genomic DNA of a plant with a restriction enzyme; (b) hybridizing a nucleic acid probe, under selective hybridization conditions, to a protease inhibitor polynucleotide sequence of said genomic DNA; (c) detecting therefrom a RFLP.

Other methods of differentiating polymorphic (allelic) variants of protease inhibitor polynucleotides can be had by utilizing molecular marker techniques well known to those of skill in the art including such techniques as: 1) single stranded conformation analysis (SSCP); 2) denaturing gradient gel electrophoresis (DGGE); 3) RNase protection assays;  
5 4) allele-specific oligonucleotides (ASOs); 5) the use of proteins which recognize nucleotide mismatches, such as the *E. coli* mutS protein; and 6) allele-specific PCR.

Other approaches based on the detection of mismatches between the two complementary DNA strands include clamped denaturing gel electrophoresis (CDGE); heteroduplex analysis (HA); and chemical mismatch cleavage (CMC). Exemplary polymorphic  
10 variants are provided in Table I, *supra*. Thus, the present invention further provides a method of genotyping comprising the steps of contacting, under stringent hybridization conditions, a sample suspected of comprising a protease inhibitor polynucleotide with a nucleic acid probe. Generally, the sample is a plant sample; preferably, a sample suspected of comprising a maize protease inhibitor polynucleotide (e.g., gene, mRNA).

15 The nucleic acid probe selectively hybridizes, under stringent conditions, to a subsequence of a protease inhibitor polynucleotide comprising a polymorphic marker. Selective hybridization of the nucleic acid probe to the polymorphic marker nucleic acid sequence yields a hybridization complex. Detection of the hybridization complex indicates the presence of that polymorphic marker in the sample. In preferred  
20 embodiments, the nucleic acid probe comprises a protease inhibitor polynucleotide.

#### **Detection of Protease Inhibitor Nucleic Acids**

The present invention further provides methods for detecting protease inhibitor polynucleotides of the present invention in a nucleic acid sample suspected of  
25 comprising a protease inhibitor polynucleotide, such as a plant cell lysate, particularly a lysate of corn. In some embodiments, a protease inhibitor gene or portion thereof can be amplified prior to the step of contacting the nucleic acid sample with a protease inhibitor polynucleotide. The nucleic acid sample is contacted with the protease inhibitor polynucleotide to form a hybridization complex. The protease inhibitor polynucleotide  
30 hybridizes under stringent conditions to a gene encoding a protease inhibitor polypeptide. Formation of the hybridization complex is used to detect a gene encoding a protease inhibitor polypeptide in the nucleic acid sample. Those of skill will appreciate that an

isolated nucleic acid comprising a protease inhibitor polynucleotide should lack cross-hybridizing sequences with non-protease inhibitor genes that would yield a false positive result.

Detection of the hybridization complex can be achieved using any number of well known methods. For example, the nucleic acid sample, or a portion thereof, may be assayed by hybridization formats including but not limited to, solution phase, solid phase, mixed phase, or *in situ* hybridization assays. Briefly, in solution (or liquid) phase hybridizations, both the target nucleic acid and the probe or primer are free to interact in the reaction mixture. In solid phase hybridization assays, probes or primers are typically linked to a solid support where they are available for hybridization with target nucleic in solution. In mixed phase, nucleic acid intermediates in solution hybridize to target nucleic acids in solution as well as to a nucleic acid linked to a solid support. In *in situ* hybridization, the target nucleic acid is liberated from its cellular surroundings in such as to be available for hybridization within the cell while preserving the cellular morphology for subsequent interpretation and analysis. The following articles provide an overview of the various hybridization assay formats: Singer *et al.*, Biotechniques 4(3): 230-250 (1986); Haase *et al.*, *Methods in Virology*, Vol. VII, pp. 189-226 (1984); Wilkinson, The theory and practice of *in situ* hybridization in: *In situ Hybridization*, D.G. Wilkinson, Ed., IRL Press, Oxford University Press, Oxford; and *Nucleic Acid Hybridization: A Practical Approach*, Hames, B.D. and Higgins, S.J., Eds., IRL Press (1987).

### **Nucleic Acid Labels and Detection Methods**

The means by which protease inhibitor nucleic acids are labeled is not a critical aspect of the present invention and can be accomplished by any number of methods currently known or later developed. Detectable labels suitable for use in the present invention include any composition detectable by spectroscopic, radioisotopic, photochemical, biochemical, immunochemical, electrical, optical or chemical means. Useful labels in the present invention include biotin for staining with labeled streptavidin conjugate, magnetic beads, fluorescent dyes (*e.g.*, fluorescein, texas red, rhodamine, green fluorescent protein, and the like), radiolabels (*e.g.*,  $^3\text{H}$ ,  $^{125}\text{I}$ ,  $^{35}\text{S}$ ,  $^{14}\text{C}$ , or  $^{32}\text{P}$ ), enzymes (*e.g.*, horse radish peroxidase, alkaline phosphatase and others commonly used in an ELISA),

and colorimetric labels such as colloidal gold or colored glass or plastic (*e.g.*, polystyrene, polypropylene, latex, etc.) beads.

Protease inhibitor nucleic acids can be labeled by any one of several methods typically used to detect the presence of hybridized nucleic acids. One common method of detection is the use of autoradiography using probes labeled with  $^3\text{H}$ ,  $^{125}\text{I}$ ,  $^{35}\text{S}$ ,  $^{14}\text{C}$ , or  $^{32}\text{P}$ , or the like. The choice of radio-active isotope depends on research preferences due to ease of synthesis, stability, and half lives of the selected isotopes. Other labels include ligands which bind to antibodies labeled with fluorophores, chemiluminescent agents, and enzymes. Alternatively, probes can be conjugated directly with labels such as fluorophores, chemiluminescent agents or enzymes. The choice of label depends on sensitivity required, ease of conjugation with the probe, stability requirements, and available instrumentation. Labeling the protease inhibitor nucleic acids is readily achieved such as by the use of labeled PCR primers.

In some embodiments, the label is simultaneously incorporated during the amplification step in the preparation of the nucleic acids. Thus, for example, polymerase chain reaction (PCR) with labeled primers or labeled nucleotides will provide a labeled amplification product. In another embodiment, transcription amplification using a labeled nucleotide (*e.g.*, fluorescein-labeled UTP and/or CTP) incorporates a label into the transcribed nucleic acids.

Non-radioactive probes are often labeled by indirect means. For example, a ligand molecule is covalently bound to the probe. The ligand then binds to an anti-ligand molecule which is either inherently detectable or covalently bound to a detectable signal system, such as an enzyme, a fluorophore, or a chemiluminescent compound. Enzymes of interest as labels will primarily be hydrolases, such as phosphatases, esterases and glycosidases, or oxidoreductases, particularly peroxidases. Fluorescent compounds include fluorescein and its derivatives, rhodamine and its derivatives, dansyl, umbelliferone, etc. Chemiluminescers include luciferin, and 2,3-dihydrophthalazinediones, *e.g.*, luminol. Ligands and anti-ligands may be varied widely. Where a ligand has a natural anti-ligand, namely ligands such as biotin, thyroxine, and cortisol, it can be used in conjunction with its labeled, naturally occurring anti-ligands. Alternatively, any haptenic or antigenic compound can be used in combination with an antibody.

Probes can also be labeled by direct conjugation with a label. For example, cloned DNA probes have been coupled directly to horseradish peroxidase or alkaline phosphatase, (Renz. M., and Kurz, K., *A Colorimetric Method for DNA Hybridization*, Nucl. Acids Res. 12: 3435-3444 (1984)) and synthetic oligonucleotides have been coupled directly with alkaline phosphatase (Jablonski, E., *et al.*, *Preparation of Oligodeoxynucleotide-Alkaline Phosphatase Conjugates and Their Use as Hybridization Probes*, Nuc. Acids. Res. 14: 6115-6128 (1986); and Li P., *et al.*, *Enzyme-linked Synthetic Oligonucleotide probes: Non-Radioactive Detection of Enterotoxigenic Escherichia Coli in Faeca Specimens*, Nucl. Acids Res. 15: 5275-5287 (1987)).

Means of detecting such labels are well known to those of skill in the art. Thus, for example, radiolabels may be detected using photographic film or scintillation counters, fluorescent markers may be detected using a photodetector to detect emitted light. Enzymatic labels are typically detected by providing the enzyme with a substrate and detecting the reaction product produced by the action of the enzyme on the substrate, and colorimetric labels are detected by simply visualizing the colored label.

### **Antibodies to Protease inhibitor Proteins**

Antibodies can be raised to a protease inhibitor protein of the present invention, including individual, allelic, strain, or species variants, and fragments thereof, both in their naturally occurring (full-length) forms and in recombinant forms. Additionally, antibodies are raised to these proteins in either their native configurations or in non-native configurations. Anti-idiotypic antibodies can also be generated. Many methods of making antibodies are known to persons of skill. The following discussion is presented as a general overview of the techniques available; however, one of skill will recognize that many variations upon the following methods are known.

A number of immunogens are used to produce antibodies specifically reactive with a protease inhibitor protein. An isolated recombinant, synthetic, or native protease inhibitor protein of 5 amino acids in length or greater and selected from a protein encoded by a protease inhibitor polynucleotide, such as exemplary sequences of SEQ ID NOS: 2,4,5,6,10, and 12, are the preferred immunogens (antigen) for the production of monoclonal or polyclonal antibodies. Those of skill will readily understand that the protease inhibitor proteins of the present invention are typically denatured prior to



formation of antibodies for screening expression libraries or other assays in which a putative protease inhibitor protein is expressed or denatured in a non-native secondary, tertiary, or quaternary structure. Naturally occurring protease inhibitor polypeptides can be used either in pure or impure form.

5                   The protease inhibitor protein is then injected into an animal capable of producing antibodies. Either monoclonal or polyclonal antibodies can be generated for subsequent use in immunoassays to measure the presence and quantity of the protease inhibitor protein. Methods of producing polyclonal antibodies are known to those of skill in the art. In brief, an immunogen (antigen), preferably a purified protease inhibitor  
10   protein, an protease inhibitor protein coupled to an appropriate carrier (*e.g.*, GST, keyhole limpet hemanocyanin, *etc.*), or an protease inhibitor protein incorporated into an immunization vector such as a recombinant vaccinia virus (*see*, U.S. Patent No. 4,722,848) is mixed with an adjuvant and animals are immunized with the mixture. The animal's immune response to the immunogen preparation is monitored by taking test  
15   bleeds and determining the titer of reactivity to the protease inhibitor protein of interest. When appropriately high titers of antibody to the immunogen are obtained, blood is collected from the animal and antisera are prepared. Further fractionation of the antisera to enrich for antibodies reactive to the protease inhibitor protein is performed where desired (*See, e.g.*, Coligan, *Current Protocols in Immunology*, Wiley/Greene, NY (1991);  
20   and Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Press, NY (1989)).

                  Antibodies, including binding fragments and single chain recombinant versions thereof, against predetermined fragments of protease inhibitor protein are raised by immunizing animals, *e.g.*, with conjugates of the fragments with carrier proteins as  
25   described above. Typically, the immunogen of interest is a protease inhibitor protein of at least about 5 amino acids, more typically the protease inhibitor protein is 10 amino acids in length, preferably, 15 amino acids in length and more preferably the protease inhibitor protein is 20 amino acids in length or greater. The peptides are typically coupled to a carrier protein (*e.g.*, as a fusion protein), or are recombinantly expressed in an  
30   immunization vector. Antigenic determinants on peptides to which antibodies bind are typically 3 to 10 amino acids in length.

Monoclonal antibodies are prepared from cells secreting the desired antibody. Monoclonal antibodies are screened for binding to a protease inhibitor protein from which the immunogen was derived. Specific monoclonal and polyclonal antibodies will usually have an antibody binding site with an affinity constant for its cognate monovalent antigen at least between  $10^6$ - $10^7$ , usually at least  $10^8$ , preferably at least  $10^9$ , more preferably at least  $10^{10}$ , and most preferably at least  $10^{11}$  liters/mole.

In some instances, it is desirable to prepare monoclonal antibodies from various mammalian hosts, such as mice, rodents, primates, humans, *etc.* Description of techniques for preparing such monoclonal antibodies are found in, *e.g.*, *Basic and Clinical Immunology*, 4th ed., Stites *et al.*, Eds., Lange Medical Publications, Los Altos, CA, and references cited therein; Harlow and Lane, *Supra*; Goding, *Monoclonal Antibodies: Principles and Practice*, 2nd ed., Academic Press, New York, NY (1986); and Kohler and Milstein, *Nature* 256: 495-497 (1975). Summarized briefly, this method proceeds by injecting an animal with an immunogen comprising a protease inhibitor protein. The animal is then sacrificed and cells taken from its spleen, which are fused with myeloma cells. The result is a hybrid cell or "hybridoma" that is capable of reproducing *in vitro*. The population of hybridomas is then screened to isolate individual clones, each of which secrete a single antibody species to the immunogen. In this manner, the individual antibody species obtained are the products of immortalized and cloned single B cells from the immune animal generated in response to a specific site recognized on the immunogenic substance.

Other suitable techniques involve selection of libraries of recombinant antibodies in phage or similar vectors (*see, e.g.*, Huse *et al.*, *Science* 246: 1275-1281 (1989); and Ward, *et al.*, *Nature* 341: 544-546 (1989); and Vaughan *et al.*, *Nature Biotechnology*, 14: 309-314 (1996)). Alternatively, high avidity human monoclonal antibodies can be obtained from transgenic mice comprising fragments of the unrearranged human heavy and light chain Ig loci (*i.e.*, minilocus transgenic mice). Fishwild *et al.*, *Nature Biotech.*, 14: 845-851 (1996). Also, recombinant immunoglobulins may be produced. See, Cabilly, U.S. Patent No. 4,816,567; and Queen *et al.*, *Proc. Nat'l Acad. Sci.* 86: 10029-10033 (1989).

The antibodies of this invention are also used for affinity chromatography in isolating protease inhibitor protein. Columns are prepared, *e.g.*, with the antibodies

linked to a solid support, *e.g.*, particles, such as agarose, Sephadex, or the like, where a cell lysate is passed through the column, washed, and treated with increasing concentrations of a mild denaturant, whereby purified protease inhibitor protein are released.

5           The antibodies can be used to screen expression libraries for particular expression products such as normal or abnormal human protease inhibitor protein. Usually the antibodies in such a procedure are labeled with a moiety allowing easy detection of presence of antigen by antibody binding.

10           Antibodies raised against protease inhibitor protein can also be used to raise anti-idiotypic antibodies. These are useful for detecting or diagnosing various pathological conditions related to the presence of the respective antigens.

          Frequently, the protease inhibitor proteins and antibodies will be labeled by joining, either covalently or non-covalently, a substance which provides for a detectable signal. A wide variety of labels and conjugation techniques are known and are  
15       reported extensively in both the scientific and patent literature. Suitable labels include radionucleotides, enzymes, substrates, cofactors, inhibitors, fluorescent moieties, chemiluminescent moieties, magnetic particles, and the like.

### **Protease Inhibitor Protein Immunoassays**

20           Means of detecting the protease inhibitor proteins of the present invention are not critical aspects of the present invention. In a preferred embodiment, the protease inhibitor proteins are detected and/or quantified using any of a number of well recognized immunological binding assays (*see, e.g.*, U.S. Patents 4,366,241; 4,376,110; 4,517,288; and 4,837,168). For a review of the general immunoassays, see also *Methods in Cell*  
25       *Biology*, Vol. 37: *Antibodies in Cell Biology*, Asai, Ed., Academic Press, Inc. New York (1993); *Basic and Clinical Immunology* 7th Edition, Stites & Terr, Eds. (1991).

          Moreover, the immunoassays of the present invention can be performed in any of several configurations, *e.g.*, those reviewed in *Enzyme Immunoassay*, Maggio, Ed., CRC Press, Boca Raton, Florida (1980); Tijan, *Practice and Theory of Enzyme Immunoassays*,  
30       *Laboratory Techniques in Biochemistry and Molecular Biology*, Elsevier Science Publishers B.V., Amsterdam (1985); Harlow and Lane, *supra*; *Immunoassay: A Practical Guide*, Chan, Ed., Academic Press, Orlando, FL (1987); *Principles and Practice of*

*Immunoassays*, Price and Newman Eds., Stockton Press, NY (1991); and *Non-isotopic Immunoassays*, Ngo, Ed., Plenum Press, NY (1988). Immunological binding assays (or immunoassays) typically utilize a "capture agent" to specifically bind to and often immobilize the analyte (in this case protease inhibitor protein). The capture agent is a moiety that specifically binds to the analyte. In a preferred embodiment, the capture agent is an antibody that specifically binds a protease inhibitor protein(s). The antibody (anti-protease inhibitor protein antibody) may be produced by any of a number of means known to those of skill in the art as described herein.

Immunoassays also often utilize a labeling agent to specifically bind to and label the binding complex formed by the capture agent and the analyte. The labeling agent may itself be one of the moieties comprising the antibody/analyte complex. Thus, the labeling agent may be a labeled protease inhibitor protein or a labeled anti-protease inhibitor protein antibody. Alternatively, the labeling agent may be a third moiety, such as another antibody, that specifically binds to the antibody/protease inhibitor protein complex.

In a preferred embodiment, the labeling agent is a second protease inhibitor protein antibody bearing a label. Alternatively, the second protease inhibitor protein antibody may lack a label, but it may, in turn, be bound by a labeled third antibody specific to antibodies of the species from which the second antibody is derived. The second can be modified with a detectable moiety, such as biotin, to which a third labeled molecule can specifically bind, such as enzyme-labeled streptavidin.

Other proteins capable of specifically binding immunoglobulin constant regions, such as protein A or protein G may also be used as the label agent. These proteins are normal constituents of the cell walls of streptococcal bacteria. They exhibit a strong non-immunogenic reactivity with immunoglobulin constant regions from a variety of species (See, generally Kronval, *et al.*, J. Immunol. 111: 1401-1406 (1973), and Akerstrom, *et al.*, J. Immunol. 135: 2589-2542 (1985)).

Throughout the assays, incubation and/or washing steps may be required after each combination of reagents. Incubation steps can vary from about 5 seconds to several hours, preferably from about 5 minutes to about 24 hours. However, the incubation time will depend upon the assay format, analyte, volume of solution, concentrations, and the like. Usually, the assays will be carried out at ambient

temperature, although they can be conducted over a range of temperatures, such as 10°C to 40°C.

While the details of the immunoassays of the present invention may vary with the particular format employed, the method of detecting an protease inhibitor protein in a biological sample generally comprises the steps of contacting the biological sample with an antibody which specifically reacts, under immunologically reactive conditions, to the protease inhibitor protein. The antibody is allowed to bind to the protease inhibitor protein under immunologically reactive conditions, and the presence of the bound antibody is detected directly or indirectly.

#### *A. Non-Competitive Assay Formats*

Immunoassays for detecting protease inhibitor proteins of the present invention include competitive and noncompetitive formats. Noncompetitive immunoassays are assays in which the amount of captured analyte (in this case protease inhibitor protein) is directly measured. In one preferred "sandwich" assay, for example, the capture agent (anti-protease inhibitor protein antibodies) can be bound directly to a solid substrate where they are immobilized. These immobilized antibodies then capture protease inhibitor protein present in the test sample. The protease inhibitor protein thus immobilized is then bound by a labeling agent, such as a second human protease inhibitor protein antibody bearing a label. Alternatively, the second protease inhibitor protein antibody may lack a label, but it may, in turn, be bound by a labeled third antibody specific to antibodies of the species from which the second antibody is derived. The second can be modified with a detectable moiety, such as biotin, to which a third labeled molecule can specifically bind, such as enzyme-labeled streptavidin.

#### *B. Competitive Assay Formats*

In competitive assays, the amount of analyte (protease inhibitor protein) present in the sample is measured indirectly by measuring the amount of an added (exogenous) analyte (protease inhibitor protein) displaced (or competed away) from a capture agent (anti protease inhibitor protein antibody) by the analyte present in the sample. In one competitive assay, a known amount of, in this case, protease inhibitor protein is added to the sample and the sample is then contacted with a capture agent, in

this case an antibody that specifically binds protease inhibitor protein. The amount of protease inhibitor protein bound to the antibody is inversely proportional to the concentration of protease inhibitor protein present in the sample.

In a particularly preferred embodiment, the antibody is immobilized on a solid substrate. The amount of protease inhibitor protein bound to the antibody may be determined either by measuring the amount of protease inhibitor protein present in an protease inhibitor protein/antibody complex, or alternatively by measuring the amount of remaining uncomplexed protease inhibitor protein. The amount of protease inhibitor protein may be detected by providing a labeled protease inhibitor protein molecule.

A hapten inhibition assay is another preferred competitive assay. In this assay a known analyte, in this case protease inhibitor protein is immobilized on a solid substrate. A known amount of anti-protease inhibitor protein antibody is added to the sample, and the sample is then contacted with the immobilized protease inhibitor protein. In this case, the amount of anti-protease inhibitor protein antibody bound to the immobilized protease inhibitor protein is inversely proportional to the amount of protease inhibitor protein present in the sample. Again, the amount of immobilized antibody may be detected by detecting either the immobilized fraction of antibody or the fraction of the antibody that remains in solution. Detection may be direct where the antibody is labeled or indirect by the subsequent addition of a labeled moiety that specifically binds to the antibody as described above.

### *C. Generation of pooled antisera for use in immunoassays*

A protease inhibitor protein that specifically binds to or that is specifically immunoreactive with an antibody generated against a defined immunogen, such as an immunogen consisting of the amino acid sequence of SEQ ID NOS: 2,4,5,6,10, and 12, is determined in an immunoassay. The immunoassay uses a polyclonal antiserum which was raised to a protein encoded by a protease inhibitor (the immunogenic polypeptide). This antiserum is selected to have low crossreactivity against other protease inhibitor proteins and any such crossreactivity is removed by immunoabsorbtion prior to use in the immunoassay (*e.g.*, by immunosorbtion of the antisera with a protease inhibitor protein of different substrate specificity and/or a protease inhibitor protein with the same substrate specificity but of a different form).

In order to produce antisera for use in an immunoassay, a protease inhibitor polypeptide (e.g., SEQ ID NOS: 2,4,5,6,10,and 12) is isolated as described herein. For example, recombinant protein can be produced in a mammalian or other eukaryotic cell line. An inbred strain of mice is immunized with the protease inhibitor protein of using a standard adjuvant, such as Freund's adjuvant, and a standard mouse immunization protocol (see Harlow and Lane, *supra*). Alternatively, a synthetic polypeptide derived from the sequences disclosed herein and conjugated to a carrier protein is used as an immunogen. Polyclonal sera are collected and titered against the immunogenic polypeptide in an immunoassay, for example, a solid phase immunoassay with the immunogen immobilized on a solid support. Polyclonal antisera with a titer of  $10^4$  or greater are selected and tested for their cross reactivity against protease inhibitor polypeptides of different forms or substrate specificity, using a competitive binding immunoassay such as the one described in Harlow and Lane, *supra*, at pages 570-573. Preferably, two or more distinct forms of protease inhibitor polypeptides are used in this determination. These distinct types of protease inhibitor polypeptides are used as competitors to identify antibodies which are specifically bound by the protease inhibitor polypeptide being assayed for. The competitive protease inhibitor polypeptides can be produced as recombinant proteins and isolated using standard molecular biology and protein chemistry techniques as described herein.

Immunoassays in the competitive binding format are used for crossreactivity determinations. For example, the immunogenic polypeptide is immobilized to a solid support. Proteins added to the assay compete with the binding of the antisera to the immobilized antigen. The ability of the above proteins to compete with the binding of the antisera to the immobilized protein is compared to the immunogenic polypeptide. The percent crossreactivity for the above proteins is calculated, using standard calculations. Those antisera with less than 10% crossreactivity with a distinct form of a protease inhibitor polypeptide are selected and pooled. The cross-reacting antibodies are then removed from the pooled antisera by immunoabsorbtion with a distinct form of a protease inhibitor polypeptide.

The immunoabsorbed and pooled antisera are then used in a competitive binding immunoassay as described herein to compare a second "target" polypeptide to the immunogenic polypeptide. In order to make this comparison, the two polypeptides are

each assayed at a wide range of concentrations and the amount of each polypeptide required to inhibit 50% of the binding of the antisera to the immobilized protein is determined using standard techniques. If the amount of the target polypeptide required is less than twice the amount of the immunogenic polypeptide that is required, then the target polypeptide is said to specifically bind to an antibody generated to the immunogenic protein. As a final determination of specificity, the pooled antisera is fully immunosorbed with the immunogenic polypeptide until no binding to the polypeptide used in the immunosorbition is detectable. The fully immunosorbed antisera is then tested for reactivity with the test polypeptide. If no reactivity is observed, then the test polypeptide is specifically bound by the antisera elicited by the immunogenic protein.

#### *D. Other Assay Formats*

In a particularly preferred embodiment, Western blot (immunoblot) analysis is used to detect and quantify the presence of protease inhibitor protein in the sample. The technique generally comprises separating sample proteins by gel electrophoresis on the basis of molecular weight, transferring the separated proteins to a suitable solid support, (such as a nitrocellulose filter, a nylon filter, or derivatized nylon filter), and incubating the sample with the antibodies that specifically bind protease inhibitor protein. The anti-protease inhibitor protein antibodies specifically bind to protease inhibitor protein on the solid support. These antibodies may be directly labeled or alternatively may be subsequently detected using labeled antibodies (*e.g.*, labeled sheep anti-mouse antibodies) that specifically bind to the anti-protease inhibitor protein.

#### *E. Quantification of Protease inhibitor Proteins.*

Protease inhibitor proteins may be detected and quantified by any of a number of means well known to those of skill in the art. These include analytic biochemical methods such as electrophoresis, capillary electrophoresis, high performance liquid chromatography (HPLC), thin layer chromatography (TLC), hyperdiffusion chromatography, and the like, and various immunological methods such as fluid or gel precipitin reactions, immunodiffusion (single or double), immunoelectrophoresis, radioimmunoassays (RIAs), enzyme-linked immunosorbent assays (ELISAs), immunofluorescent assays, and the like.



#### *F. Reduction of Non-Specific Binding*

One of skill will appreciate that it is often desirable to reduce non-specific binding in immunoassays and during analyte purification. Where the assay involves an antigen, antibody, or other capture agent immobilized on a solid substrate, it is desirable to minimize the amount of non-specific binding to the substrate. Means of reducing such non-specific binding are well known to those of skill in the art. Typically, this involves coating the substrate with a proteinaceous composition. In particular, protein compositions such as bovine serum albumin (BSA), nonfat powdered milk, and gelatin are widely used.

#### *G. Immunoassay Labels*

The labeling agent can be, *e.g.*, a monoclonal antibody, a polyclonal antibody, a binding protein or complex, or a polymer such as an affinity matrix, carbohydrate or lipid. Detectable labels suitable for use in the present invention include any composition detectable by spectroscopic, radioisotopic, photochemical, biochemical, immunochemical, electrical, optical or chemical means. Detection may proceed by any known method, such as immunoblotting, western analysis, gel-mobility shift assays, fluorescent *in situ* hybridization analysis (FISH), tracking of radioactive or bioluminescent markers, nuclear magnetic resonance, electron paramagnetic resonance, stopped-flow spectroscopy, column chromatography, capillary electrophoresis, or other methods which track a molecule based upon an alteration in size and/or charge. The particular label or detectable group used in the assay is not a critical aspect of the invention. The detectable group can be any material having a detectable physical or chemical property. Such detectable labels have been well-developed in the field of immunoassays and, in general, any label useful in such methods can be applied to the present invention. Thus, a label is any composition detectable by spectroscopic, photochemical, biochemical, immunochemical, electrical, optical or chemical means. Useful labels in the present invention include magnetic beads, fluorescent dyes, radiolabels, enzymes, and colorimetric labels or colored glass or plastic beads, as discussed for nucleic acid labels, *supra*.

The label may be coupled directly or indirectly to the desired component of the assay according to methods well known in the art. As indicated above, a wide variety of labels may be used, with the choice of label depending on the sensitivity required, ease of conjugation of the compound, stability requirements, available  
5 instrumentation, and disposal provisions.

Non-radioactive labels are often attached by indirect means. Generally, a ligand molecule (*e.g.*, biotin) is covalently bound to the molecule. The ligand then binds to an anti-ligand (*e.g.*, streptavidin) molecule which is either inherently detectable or covalently bound to a signal system, such as a detectable enzyme, a fluorescent  
10 compound, or a chemiluminescent compound. A number of ligands and anti-ligands can be used. Where a ligand has a natural anti-ligand, for example, biotin, thyroxine, and cortisol, it can be used in conjunction with the labeled, naturally occurring anti-ligands. Alternatively, any haptenic or antigenic compound can be used in combination with an antibody.

15 The molecules can also be conjugated directly to signal generating compounds, *e.g.*, by conjugation with an enzyme or fluorophore. Enzymes of interest as labels will primarily be hydrolases, particularly phosphatases, esterases and glycosidases, or oxidoreductases, particularly peroxidases. Fluorescent compounds include fluorescein and its derivatives, rhodamine and its derivatives, dansyl, umbelliferone, etc.  
20 Chemiluminescent compounds include luciferin, and 2,3-dihydrophthalazinediones, *e.g.*, luminol. For a review of various labelling or signal producing systems which may be used, see, U.S. Patent No. 4,391,904, which is incorporated herein by reference.

Means of detecting labels are well known to those of skill in the art. Thus, for example, where the label is a radioactive label, means for detection include a  
25 scintillation counter or photographic film as in autoradiography. Where the label is a fluorescent label, it may be detected by exciting the fluorochrome with the appropriate wavelength of light and detecting the resulting fluorescence, *e.g.*, by microscopy, visual inspection, via photographic film, by the use of electronic detectors such as charge coupled devices (CCDs) or photomultipliers and the like. Similarly, enzymatic labels  
30 may be detected by providing appropriate substrates for the enzyme and detecting the resulting reaction product. Finally, simple colorimetric labels may be detected simply by

observing the color associated with the label. Thus, in various dipstick assays, conjugated gold often appears pink, while various conjugated beads appear the color of the bead.

Some assay formats do not require the use of labeled components. For instance, agglutination assays can be used to detect the presence of the target antibodies.

5 In this case, antigen-coated particles are agglutinated by samples comprising the target antibodies. In this format, none of the components need be labeled and the presence of the target antibody is detected by simple visual inspection.

#### **Assays for Compounds that Modulate Protease Inhibitory Activity or Expression**

10 The present invention also provides means for identifying compounds that bind to (e.g., substrates), and/or increase or decrease (i.e., modulate) the inhibitory activity of, protease inhibitor polypeptides. The method comprises contacting a protease inhibitor polypeptide of the present invention with a compound whose ability to bind to or modulate inhibitory activity is to be determined. The protease inhibitor polypeptide  
15 employed will have at least 20%, preferably at least 30% or 40%, more preferably at least 50% or 60%, and most preferably at least 70% or 80% of the inhibitory activity of the full-length (native and endogenous) protease inhibitor polypeptide. Generally, the protease inhibitor polypeptide will be present in a range sufficient to determine the effect of the compound, typically about 1 nM to 10  $\mu$ M. Likewise, the compound will be  
20 present in a concentration of from about 1 nM to 10  $\mu$ M. Those of skill will understand that such factors as enzyme concentration, ligand concentrations (i.e., substrates, products, inhibitors, activators), pH, ionic strength, and temperature will be controlled so as to obtain useful kinetic data and determine the presence or absence of a compound that binds or modulates protease inhibitor polypeptide activity. Methods of measuring  
25 enzyme kinetics is well known in the art. See, e.g., Segel, *Biochemical Calculations*, 2<sup>nd</sup> ed., John Wiley and Sons, New York (1976).

Although the present invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be obvious that certain changes and modifications may be practiced within the scope of the appended  
30 claims.

**Example 1: Isolation of DNA Coding for Protease inhibitor Protein from *Zea mays* or other plant library**

The polynucleotides having DNA sequences given in SEQ ID Nos: 15, 17, 19, 21, and 23  
5 were obtained from the sequencing of cDNA clones prepared from maize.

SEQ ID NO 15 is a contig comprised of 28 cDNA clones. 20 of the cDNA clones were  
from libraries prepared from leaves treated with jasmonic acid. One was from a root  
library. Four were from libraries prepared from corn rootworm-infested roots. One was  
from a tassel library. One was from a library prepared from seedlings recovering from  
10 heat shock. One was from a shoot culture library.

SEQ ID NO 17 is a contig comprised of two cDNA clones. One was from a jasmonic acid  
treated leaf library. The other was from an induced resistance leaf library.

SEQ ID NO 19 is a contig comprised of two cDNA clones. One was from a germinating  
maize seedling library. The other was from jasmonic acid treated leaf library.

15 SEQ ID NO 21 is a contig comprised of 4 cDNA clones. All four were from libraries  
prepared from jasmonic acid treated leaves.

SEQ ID NO 5 is a contig comprised of two cDNA clones. One was from a library  
prepared from silks, 24 hours post pollination. The other was from a library prepared  
from root tips less than 5 mm in length.

20 One skilled in the art could apply these same methods to other plant nucleotide containing  
libraries.

**Example 2: Engineering BHL for nutritional enhancement**

Wild type CI-2 (from barley) contains 49.4% essential amino acids (41/83) and  
9.6% lysine (8/83). Using the strategies outlined below, six different BHL variants with  
30 increasing amounts of lysine have been proposed. The lysine percentages are 21.5%,  
24.1%, 23.1%, and 25.3%, for BHL-1, BHL-1N, BHL-2, BHL-2N, BHL-3, and BHL-3N,  
respectively. Construct BHL-1N contains the same eight substitutions as BHL-1, plus  
lysine substitutions in the 18 additional amino acid residues in the amino terminal  
region. BHL-2 is the same as BHL-1 but with changes of amino acid residues 40 and 42

to Ala and amino acid residue 47 to lysine. Construct BHL-2N contains the same 11 substitutions as BHL-2, plus four lysine substitutions in the 18 additional amino acid residues in the amino terminal region. BHL-3 is the same as BHL-2 except that residues 40 and 42 are changed to Gly and His, respectively. Construct BHL-3N contains the same 11 substitutions as BHL-3, plus the four lysine substitutions in 18 additional amino acid residues in the amino terminal region. One skilled in the art will realize that essential and non-wild-type amino acid residue substitutions will be tolerated at both the same positions substituted with lysine, and at other positions.

The active site loop region encompasses an extended loop region from about amino acid residue 53 to about amino acid residue 70. Destabilization of the reactive loop was achieved by substituting the non-wild type amino acids residues at about positions 53 to about 70. Amino acid residues were changed by primer mutagenesis. Preferably, the following mutations are made: Arg62 → Lys62, Arg65 → Lys65, Arg67 → Lys67, Thr58 → Ala58 or Gly58, Met59 → Lys59, and Glu60 → Ala60 or His60. However, it will be readily apparent to one skilled in the art that functionally equivalent substitutions to those described above will also be effective in the present invention.

In a preferred embodiment of the present invention, the present protein has both elevated essential amino acid content and reduced protease inhibitor activity.

Modification in the area by amino acid substitution or other means, destroys the hydrogen bonding and changes or reduces the protease inhibitor activity of BHL. Substitution of amino acid residues threonine, at position 58, and glutamic acid, at position 60, with glycine and histidine, respectively, resulted in a protein with lowered protease inhibitor activity. Residue 59 is a critical residue in modifying protease inhibitor activity and changing specificity. When this residue was changed to a lysine, the protease inhibition specificity was changed from a chymotrypsin inhibitor to a trypsin inhibitor.

The present invention provides for the creation of a nutritionally enhanced feed from WT CI-2 through at least one lysine substitution of residues 1,18,11,17,19,34,41,56,59,62,67 and 73 (long versions BHL-1N, 2N, 3N) plus residue 67 in BH2-2N and BH2-3N. Lysine substitutions in BHL-1,2 and 3 are at amino acid residues 1,16,23,41,44,49 and 55, plus residue 47 in BHL-2 and BHL-3.

### **Example 3- Construction of Expression Cassettes**

Vector construction was based upon the published WT CI-2A sequence information Williamson *et al*, Eur. J. Biochem 165: 99-106 (1987) and SEQ ID NO 13. Methods for obtaining full length or truncated wild-type CI-2 DNA include, but are not limited to PCR amplification, from a barley (or other plant ) endosperm cDNA library  
 5 using oligonucleotides derived from Seq. ID no 13 or from the published sequence *supra*, using probes derived from the same on a barley (or other plant ) endosperm cDNA library, or using a set of overlapping oligonucleotides that encompass the gene.

### *BHL-1*

10 The BHL-1 insert corresponds to SEQ ID NO 1, plus start and stop codons. Oligonucleotide pairs, N4394/N4395, and N4396/N4397, were annealed and ligated together to make a 202 base pair double stranded DNA molecule with overhangs compatible with *Rca* I and *Nhe* I restriction sites. PCR was performed on the annealed molecule using primers N5045 and N5046 to add a 5' *Spe* I site and 3' *Hind* III site. The  
 15 PCR product was then restriction digested at those sites and ligated into pBluescript II KS+ at *Spe* I and *Hind* III sites. The insert was then removed by restriction digestion with *Rca* I and *Hind* III and was ligated into the *Nco* I and *Hind* III sites of pET28a (Novagen) to form the BHL-1 construct.

20 Oligonucleotide and primer sequences (5' to 3'):  
 N4394

1 CATGAAGCTG AAGACAGAGT GGCCGGAGTT GGTGGGGAAA  
 TCGGTGGAGA

25

51 AAGCCAAGAA GGTGATCCTG AAGGACAAGC CAGAGGCGCA  
 AATCATAGTT

101 CTGC

30

N4395

1 CAACCGGCAG AACTATGATT TGCGCCTCTG GCTTGTCTT  
 CAGGATCACC

35

51 TTCTTGGCTT TCTCCACCGA TTTCCCCACC AACTCCGGCC  
 ACTCTGTCTT

101 CAGCTT

N4396

1 CGGTTGGTAC AAAGGTGACG AAGGAATATA AGATCGACCG  
 5 CGTCAAGCTC

51 TTTGTGGATA AAAAGGACAA CATCGCGCAG GTCCCCAGGG TCGG

10 N4397

1 CTAGCCGACC CTGGGGACCT GCGCGATGTT GTCCTTTTAA  
 TCCACAAAGA

15 51 GCTTGACGCG GTCGATCTTA TATTCCTTCG TCACCTTTGT AC

N5045

20 1 GTACTAGTCA TGAAGCTGAA GACAGA

N5046

25 1 GAGAAGCTTG CTAGCCGACC CTGGGGAC

b. BHL-2: The BHL-2 construct insert corresponds to SEQ ID NO 3, plus start and stop codons. An overlap PCR strategy was used to make the BHL-2 construct. PWO polymerase from Boehringer-Mannheim was used for all PCR reactions. The primers were  
 30 chosen to change 3 amino acids in the BHL-1 active site loop region, and to create unique *Age*I and *Hind* III restriction sites flanking the active site loop, to facilitate loop replacement in future constructs. A unique *Rca* I site (compatible with *Nco* I) was included at the 5' end, and a unique *Xho* I site was included at the 3' end. The overlap PCR was done as follows: PCR was done with primers N13561 and N13564, using the  
 35 BHL-1 construct as template. A separate PCR was done with primers N13563 and N13562, again using the BHL-1 construct as template. The products from both reactions were gel purified and combined. Primer N13565, which overlapped regions on both of the PCR products, was then added and another PCR was done to generate the full-length insert. The resulting product was amplified by another PCR with primers N13561 and  
 40 N13562. It was subsequently suspected that a deletion was present in N13562 that caused a frameshift near the 3' end of the PCR product. To avoid this frameshift problem, a final

PCR reaction was done with primers N13562 and N13905. The final PCR product was digested with *Rca* I and *Xho* I, and then ligated into the *Nco* I and *Xho* I sites of pET 28b.

Note: Some primers had 6-oligonucleotide extensions to improve restriction digestion efficiency.

5

Primer sequences (5' TO 3'):

N13561

1 TTTTTTTCATGAAGCTGAAGACA

N13562 (as ordered)

10 1 TTTTTTCTCGAGGCTAGCCGACCCTGGGGA

N13563

1 ATCGACAAGGTCAAGCTTTTTGTGGATAAAAAGGA

N13564

1 CACCTTTGTACCAACCGGTAGAACTATGATTTGCGC

15 N13565

1 GTTGGTACAAAGGTGGCGAAGGCCTATAAGATCGACAAGGTCAAG

N13905

1 TTTTTTCTCGAGGCTAGCCGACCCTGGGGACCTGCGCTA

20

c. BHL-3: The BHL-3 construct insert corresponds to SEQ ID NO 5, plus start and stop codons. The BHL-2 construct was digested with *Age* I and *Hind* III, and the region between these sites was removed by gel purification. Oligonucleotide pairs, N14471 and N14472, were annealed to make a double stranded DNA molecule with overhangs compatible with *Age* I and *Hind* III restriction sites. The annealed product was ligated into the *Age* I and *Hind* III sites of the digested BHL-2 construct to yield the BHL-3 construct.

25

Oligonucleotide Primer sequences (5' to 3'):

N14471

1 CCGGTTGGTACAAAGGTGGGTAAGCATTATAAGATCGACAAGGTCA

30

N14472

1 AGCTTGACCTTGTCGATCTTATAATGCTTACCCACCTTTGTACCAA

d. BHL-1N, BHL-2N, and BHL-3N

The BHL-1N, BHL-2N, and BHL-3N construct inserts correspond to SEQ ID No 9, SEQ ID NO 11, and SEQ ID NO 7, respectively, plus start and stop codons. Three separate PCR reactions were done with either the BHL-1, BHL-2, or BHL-3 constructs as template. The primers for these reactions were N13771 and N13905. The resulting PCR products were digested with *Rca* I and *Xho* I and ligated into the *Nco* I and *Xho* I sites of pET 28b to yield the BHL-1N, BHL-2N, and BHL-3N constructs.

35

Primer sequences (5' to 3'):

40

N13771



1  
 TTTTTCATGAAGTCGGTGGAGAAGAAACCGAAGGGTGTGAAGACAGG  
 50 TGCGGGTGACAAGCATAAGCTGAAGACAGAGTG  
 N13905 (already provided in BHL-2 description)

5 BHL-1N is an 83 residue polypeptide in which residues 1,8,11, and 17 were also replaced with lysine. The resulting compound has the protein sequence indicated in Sequence I.D. No.10.

BHL-2N is an 83 residue polypeptide in which residues 1,8,11, and 17 were also replaced with lysine. The resulting compound has the protein sequence indicated in  
 10 Sequence I.D. No.12.

BHL-3N is an 83 residue polypeptide in which residues 1,8,11, and 17 were also replaced with lysine. The resulting compound has the protein sequence indicated in Sequence I.D. No.8.

### 15 **Example 3 - Expression of BHL-1 in *E. coli***

#### *Expression in E. coli*

BHL-1, BHL-2, BHL-3, BHL-3N, and the truncated wild-type CI-2 (residues 19 through 65 of SEQ ID NO. 14) were expressed in *E. coli* using materials and methods from Novagen, Inc. The Novagen expression vector pET-28 was used (pET-28a for WT CI-2  
 20 and BHL-1, and pET-28b for the other proteins). *E. coli* strains BL21(DE-3) or BL21(DE-3)pLysS were used. Cultures were typically grown until an OD at 600 nm of 0.8 to 1.0, and then induced with 1 mM IPTG and grown another 2.5 to 5 hours before harvesting. Induction at an OD as low as 0.4 was also done successfully. Growth temperatures of 37 degrees centigrade and 30 degrees centigrade were both used successfully. The media  
 25 used was 2xYT plus the appropriate antibiotic at the concentration recommended in the Novagen manual.

#### *Purification*

a. WT CI-2 (truncated)-- Lysis buffer was 50 mM Tris-HCl, pH 8.0, 1 mM EDTA,  
 30 150 mM NaCl. The protein was precipitated with 70% ammonium sulfate. The pellet was dissolved and dialyzed against 50 mM Tris-HCl, pH 8.6. The protein was loaded onto a Hi-Trap Q column, and the unbound fraction was collected and precipitated in 70% ammonium sulfate. The pellet was dissolved in 50 mM sodium phosphate, pH 7.0, 200

mM NaCl, and fractionated on a Superdex-75 26/60 gel filtration column. Fractions were pooled and concentrated.

b. BHL-1--Lysis buffer was 50 mM sodium phosphate, pH 7.0, 1 mM EDTA.

The protein was loaded onto an SP Sepharose FF 16/10 column, washed with 150 mM NaCl in 50 mM sodium phosphate, pH 7.0, and then eluted with an NaCl gradient in 50 mM sodium phosphate. BHL-1 eluted at approximately 200 mM NaCl. Fractions were pooled and concentrated.

c. BHL-2, BHL-3, and BHL-3N--Lysis buffer was 50 mM Hepes, pH 8.0, 2mM EDTA, 0.1% Triton X-100, and 0.5 mg/ml lysozyme. The protein was loaded onto an SP-Sepharose cation exchange column (typically a 5 to 10 ml size), washed with 150 mM NaCl in 50 mM sodium phosphate, pH 7.0, and eluted with 500 mM NaCl in 50 mM sodium phosphate, pH 7.0. The protein was concentrated and then subjected to Superdex-75 gel filtration chromatography twice.

d. BHL-1--Lysis buffer was 50 mM sodium phosphate, pH 7.0, 1 mM EDTA. The protein was loaded onto an SP Sepharose FF 16/10 column, washed with 150 mM NaCl in 50 mM sodium phosphate, pH 7.0, and then eluted with an NaCl gradient in 50 mM sodium phosphate. BHL-1 eluted at approximately 200 mM NaCl. Fractions were pooled and concentrated.

e. BHL-2, BHL-3, and BHL-3N--Lysis buffer was 50 mM Hepes, pH 8.0, 2mM EDTA, 0.1% Triton X-100, and 0.5 mg/ml lysozyme. The protein was loaded onto an SP-Sepharose cation exchange column (typically a 5 to 10 ml size), washed with 150 mM NaCl in 50 mM sodium phosphate, pH 7.0, and eluted with 500 mM NaCl in 50 mM sodium phosphate, pH 7.0. The protein was concentrated and then subjected to Superdex-75 gel filtration chromatography twice.

#### 4. Storage

The purified proteins were stored long term by freezing in liquid nitrogen and keeping frozen at -70 degrees centigrade.

#### 5. Verification of recombinant protein identity.

##### a. DNA sequencing--

The insert region of these pET 28 constructs was confirmed by DNA sequencing.

##### b. N-terminal protein sequencing --

100 µg of purified BHL-3 were digested with 1 µg of chymotrypsin (Sigma catalog # C-4129) for 30 min at 37 degrees centigrade in 50 mM sodium phosphate, pH 7.0. The resulting chymotryptic fragments were purified by reversed phase chromatography, using an acetonitrile gradient for elution. Three pure peaks were observed and were sent to the  
5 University of Michigan Medical School Protein Structure Facility for N-terminal sequencing (6 cycles). Peak 1 had an N-terminal sequence of val-asp-lys-lys-asp-asn. Peak 2 had an N-terminal sequence of lys-ile-asp-lys-val-lys. Peak 3 had an N-terminal sequence of met-lys-leu-lys-thr-glu. These results demonstrate that chymotrypsin cleaved BHL-3 after tyr-61 and phe-69. The N-terminal sequences all match exactly the BHL-3  
10 expected sequence, assuming that the start methionine was largely retained in the recombinant protein. This experiment verifies that the protein we expressed in and purified from *E. coli* was BHL-3. Furthermore, SDS-PAGE analysis with 16.5% Tris-Tricine precast gels from Biorad showed a similar mobility of BHL-1 and BHL-2 with the confirmed BHL-3 protein, as would be expected because BHL-1 and BHL-2 have  
15 molecular masses very similar to that of BHL-3.

160 µg of BHL-3N were digested with 1.6 µg pepsin overnight, and the resulting peptic fragments were purified by reversed phase chromatography. Five of the resulting peaks were sent to the Iowa State University Protein Facility for N-terminal sequencing through four cycles. The N-terminal sequences of the 5 peaks were: val-gly-lys-ser, phe-  
20 val-asp-lys, pro-val-gly-thr, met-lys-ser-val, and ile-ile-val-leu, all of which exactly match the expected BHL-3N sequence, assuming that the start methionine was largely retained in this recombinant protein. This experiment verifies that the protein we expressed in and purified from *E. coli* was BHL-3N.

#### c. Protease inhibition--

25 The obvious protease inhibitory activity observed for BHL-1 and for the wild-type protein are further evidence that we have purified the expected proteins from *E. coli*. The details of these protease inhibition experiments are described next.

The following experiments utilized truncated wild type CI-2 as represented as nt. 55-249 in Seq. ID NO. 13 with addition of start and stop codons.

**Example 5 - Protease Inhibition assays and Proteolytic Digests**

5 a. Chymotrypsin

Protease activity was measured by an increase in absorbance at 405 nm.

Sigma Chymotrypsin type II (Bovine pancreas) Cat. # C-4129.

Substrate - Sigma cat. # 5-7388. N-Succinyl-Ala-Ala-Pro-phe-p nitro anilide or BHL protein used, 1  $\mu$ M chymotrypsin, 1mM substrate, 200  $\mu$ l volume

10 1 $\mu$ M BSA included in control (no CI-2, no BHL).

Preincubated 30 min 37° C., then added substrate to start and kept at 37° C.

Buffer 0.2M tris - HCl pH 8.0

Read Abs 405 nm - 30 min

Protease Activity - % of Control ABS. 405 nm

15

	Abs. At 405 nm			
	Rep. 1	Rep. 2	Mean (S.D.) Using % control data	
Control 1-value	0.350	0.299	.	
% control	100.0	100.0	100.0	
WT CI-2-value	.042	.018		
% control	12.0	6.0	9.0	(4.2)
BHL-1-value	.289	.274		
% control	82.6	91.6	87.1	(6.4)
BHL-2-value	.309	.318		
% control	88.3	106.4	97.4	(12.8)
BHL-3-value	.346	.315		
% control	98.9	105.4	102.2	(4.6)
BHL-3N-value	.318	.315		
% control	90.9	105.4	98.2	(10.3)

## b. Subtilisin

Subtilisin carlsberg from *Bacillus licheniformis* (Sigma cat. # P-5380)

Substrate and buffer same as for chymotrypsin exper. 200 ul reaction volume

1  $\mu$ M CI2 or BHL

5 1nM subtilisin

1mM Substrate

room temp (25° C)

30 min. preincubated then added substrate and read absorbance at 405nm

30 min. data used

10 1uM BSA used in control (no CI2 or BHL)

	Abs. At 405 nm			
	Rep. 1	Rep. 2	Mean (S.D.) Using % control data	
Control 1-value	2.171	1.834		
% control	100.0	100.0	100.0	
WT CI-2-value	.014	.002		
% control	0.6	0	0.3	(0.4)
BHL-1-value	.286	.295		
% control	13.2	16.1	14.7	(2.1)
BHL-2-value	1.692	1.569		
% control	77.9	85.6	81.8	(5.4)
BHL-3-value	7.056	1.960		
% control	94.7	106.9	100.8	(8.6)
BHL-3N-value	2.103	1.729		
% control	96.9	94.3	95.6	(1.8)

## c. Trypsin

Bovine pancreas trypsin (Sigma cat #T-8919)

Substrate S-2222 (chromogenix): N-benzoyl-2-isoleuene-L-glutamyl-glycyl-L-arginine-p-nitroaniline

5 buffer: 50mM Tris pH 7.5, 2mM NaCl, 2mM CaCl<sub>2</sub>, 0.005 % TritonX-100.

30 min. preincubation 25°, then added substrate and kept at 25°; these are 30 minute values.

1 mM substrate, 5uM CI-2 or BHL, 0.5nM trypsin, no BSA in control. 200 ul reaction volume

	Abs. At 405nm				Mean (S.D.) Using % Control Data	
	Rep. 1	Rep. 2	Rep. 3	Rep. 4		
Control 1-value	.505	.533	.473	.391		
% control	100.0	100.0	100.0	100.0	100.0	
WT CI-2-value	.561	.533	.474	.420		
% control	111.1	100.0	100.2	107.4	104.7	(5.5)
BHL-1-value	.072	.096	.041	.057		
% control	14.3	18.0	8.7	14.6	13.9	(3.9)
BHL-2-value	.436	.481	.404	.405		
% control	86.3	90.2	85.4	103.5	91.4	(8.4)
BHL-3-value	.536	.557	.456	.430		
% control	106.1	104.5	96.4	110.0	104.3	(5.7)
BHL-3N-value	.542	.583	.490	.437		
% control	107.3	109.4	103.6	111.8	108.0	(3.5)

d. Elastase

Porcine elastase Type IV (Sigma) Cat# E-0258

Substrate: Sigma S-4760 N-succinyl-ala-ala-ala-p-nitroanile

buffer: 0.2M Tris HCl pH 8.0 200 ul reactive volume 50nM elastase, 2 uM CI-2 or BHL;

5 1mM substrate

1uM BSA in control

15 min. preincub, 25°, then added substrate. Kept at 25°; 30 min. data

	Abs. At 405 nm			
	Rep. 1	Rep. 2	Mean (sp) Using % control data	
Control 1-value	1.416	1.461		
% control	100.0	100.0	100.0	
WT CI-2-value	.030	.049		
% control	2.1	3.4	2.8	(0.9)
BHL-1-value	1.519	1.459		
% control	107.3	99.9	103.6	(5.2)
BHL-2-value	1.558	1.509		
% control	110.0	103.3	106.7	(4.7)
BHL-3-value	1.587	1.493		
% control	112.1	102.2	107.2	(7.0)
BHL-3N-value	1.527	1.481		
% control	107.8	101.4	104.6	(4.5)

protease inhibition summary - % of control

Protein	Chymotrypsin	Trypsin	Elastase	Subtilisin
WT CI-2	9.0	104.7	2.8	0.3
BHL-1	87.1	13.9	103.6	14.7
BHL-2	97.4	91.4	106.7	81.8
BHL-3	102.2	104.3	107.2	100.8
BHL-3N	98.2	108.0	104.6	95.6

- 5 These experiments show that BHL-2, BHL-3 and BHL-3N have reduced protease inhibition activity compared to WT CII2.

*Digestion by trypsin*

- The purified proteins were incubated at 37 degrees centigrade with a 100:1 (wt:wt) ratio of BHL protein or wild-type CI-2 : trypsin for 15min, 30 min, 1 hr, 2 hr, or 4 hr. Incubation buffer was 50 mM sodium phosphate, pH 7.0. Bovine pancreas trypsin was used (Sigma catalog # T-8918). Digestion was assessed by SDS-PAGE with 16.5% Tris-Tricine precast gels from Biorad. The BHL-2, BHL-3, and BHL-3N proteins were digested by trypsin in 15 minutes. In contrast, the BHL-1 and wild-type truncated CI-2 proteins were resistant to trypsin. This experiment confirmed that the BHL-2, BHL-3, and BHL-3N proteins are not effective inhibitors of trypsin.

*Digestion by chymotrypsin.*

- The purified proteins were incubated at 37 degrees centigrade with a 100:1 (wt:wt) ratio of BHL protein or wild-type CI-2 : chymotrypsin for 15min, 30 min, 1 hr, 2 hr, or 4 hr. Incubation buffer was 50 mM sodium phosphate, pH 7.0. Bovine pancreas chymotrypsin type II (Sigma catalog # S-7388 was used. Digestion was assessed by SDS-PAGE with 16.5% precast Tris-Tricine gels from Biorad. BHL-2, BHL-3, and BHL-3N proteins were digested by chymotrypsin in 15 minutes. In contrast, BHL-1 and wild-type CI-2 proteins were resistant to chymotrypsin. This experiment confirmed that BHL-2, BHL-3, and BHL-3N are not effective inhibitors of chymotrypsin.

*Digestion in simulated gastric fluid.*



Simulated gastric fluid was prepared by dissolving 20 mg NaCl and 32 mg of pepsin in 70  $\mu$ l of HCl plus enough water to make 10 ml. Porcine stomach pepsin (Sigma cat # P-6887) was used. 50  $\mu$ l of 1 mg/ml BHL-3N or wild-type CI-2 protein were incubated with 250  $\mu$ l simulated gastric fluid at 37 degrees centigrade. At 15 sec, 30 sec, 5 1 min, 5 min, and 30 min, 40  $\mu$ l aliquots were removed to a stop solution consisting of 40  $\mu$ l 2X Tris-Tricine SDS sample buffer (Biorad) that also contained 3  $\mu$ l of 1 M Tris-HCl, pH 8.0 and 0.1 mg/ml pepstatin A (Boehringer-Mannheim cat # 60010). Digestion was assessed by 16.5% Tris-Tricine SDS-PAGE (precast gels from Biorad).

10 Both BHL-3N and wild-type CI-2 were digested in simulated gastric fluid in 15 seconds. This experiment suggests that our engineered proteins and even the wild-type protein would likely be digested into proteolytic fragments in the stomach of humans or monogastric animals.

15 *Digestion in simulated intestinal fluid.*

Simulated intestinal fluid was prepared by dissolving 68 mg of monobasic potassium phosphate in 2.5 ml of water, adding 1.9 ml of 0.2 N sodium hydroxide and 4 ml of water. Then 2.0 g porcine pancreatin (Sigma catalog # P-7545) was added and the resulting solution was adjusted with 0.2N sodium hydroxide to a pH of 7.5. Water was 20 added to make a final volume of 10 ml.

50  $\mu$ g of BHL-3N or wild-type CI-2 protein in 50  $\mu$ l were incubated with 250  $\mu$ l simulated intestinal fluid at 37 degrees centigrade . At 15 sec, 30 sec, 1 min, 5 min, and 30 min, 40  $\mu$ l aliquots were removed and added to 40  $\mu$ l of a stop solution consisting of 25 2X Tris-Tricine SDS sample buffer (Biorad) containing 2 mM EDTA and 2mM phenylmethylsulfonyl fluoride (Sigma catalog # P-7626). Digestion was assessed by 16.5 % Tris-Tricine SDS-PAGE (precast gels form Biorad).

BHL-3N was digested by simulated intestinal fluid in 15 seconds. In contrast, 30 wild-type CI-2 was resistant to digestion for 30 minutes. This experiment shows that in the intestine of humans or monogastric animals, our engineered protein would likely be more digestible than the wild-type protein would be. These results are consistent with the

protease inhibition assays showing that BHL-3N was not an effective protease inhibitor. The inventive protein was digested in less than five minutes, less than one and less than 30 seconds.

5 *Digestion in simulated gastric fluid*

Simulated gastric fluid was prepared by dissolving 20 mg NaCl and 32 mg of pepsin in 70  $\mu$ l of HCl plus enough water to make 10 ml. Porcine stomach pepsin (Sigma cat # P-6887) was used. 50  $\mu$ l of 1 mg/ml BHL-3N or wild-type CI-2 were incubated with 250  $\mu$ l simulated gastric fluid at 37 degrees centigrade. At 15 sec, 30 sec, 1 min, 5  
10 min, and 30 min, 40  $\mu$ l aliquots were removed to a stop solution consisting of 40  $\mu$ l 2X Tris-Tricine SDS sample buffer (Biorad) that also contained 3  $\mu$ l of 1 M Tris-HCl, pH 8.0 and 0.1 mg/ml pepstatin A (Boehringer-Mannheim cat # 60010). Digestion was assessed by 16.5% Tris-Tricine SDS-PAGE (precast gels from Biorad ~~tm~~).

Both BHL-3N and wild-type CI-2 were digested in simulated gastric fluid in 15  
15 seconds. This experiment suggests that our engineered proteins and even the wild-type protein would likely be digested into proteolytic fragments in the stomach of humans or monogastric animals.

*Digestion in simulated intestinal fluid.*

20 Simulated intestinal fluid was prepared by dissolving 68 mg of monobasic potassium phosphate in 2.5 ml of water, adding 1.9 ml of 0.2 N sodium hydroxide and 4 ml of water. Then 2.0 g porcine pancreatin (Sigma catalog # P-7545) was added and the resulting solution was adjusted with 0.2N sodium hydroxide to a pH of 7.5. Water was added to make a final volume of 10 ml.

25 50  $\mu$ l of 1mg/ml BHL-3N or wild-type CI-2 were incubated with 250  $\mu$ l simulated intestinal fluid at 37 degrees centigrade . At 15 sec, 30 sec, 1 min, 5 min, and 30 min, 40  $\mu$ l aliquots were removed and added to 40  $\mu$ l of a stop solution consisting of 2X Tris-Tricine SDS sample buffer (Biorad) containing 2 mM EDTA and 2mM  
30 phenylmethylsulfonyl fluoride (Sigma catalog # P-7626). Digestion was assessed by 16.5 % Tris-Tricine SDS-PAGE (precast gels form Biorad).

BHL-3N was digested by simulated intestinal fluid in 15 seconds. In contrast, wild-type CI-2 was resistant to digestion for 30 minutes. This experiment shows that in the intestine of humans or monogastric animals, our engineered protein would likely be more digestible than the wild-type protein would be. These results are consistent with the

5 protease inhibition assays showing that BHL-3N was not an effective protease inhibitor. The inventive proteins were digested in less than five minutes, less than one minute and less than 30 seconds.

**Example 6 - Protein Conformation**

Wild type CI-2, BHL-1, BHL-2, BHL-3 and BHL-3N at proteins concentrations of approximately 0.16mg/ml in 10mM sodium phosphate, pH = 7.0 were prepared and sent to the University of Michigan Medical School Protein Structure Facility for circular dichroism analysis. Data indicates that the substituted proteins BHL-1, BHL-2 and BHL-3 have very similar CD spectra confirming that the BHL proteins fold into a structure similar to the wild type CI-2.

**Example 7 - Thermodynamic stability**

Equilibrium denaturation experiments were done to assess the thermodynamic stability of the engineered and wild-type proteins, following the method of Pace et al. (Meth. Enzym. 131:266-280). The engineered or wild-type proteins at a concentration of 2  $\mu$ M were incubated 18 hours at 25 degrees centigrade in 10 mM sodium phosphate, pH 7.0, with various concentrations of guanidine-hydrochloride. Unfolding of the proteins was monitored by measuring intrinsic fluorescence at 25 degrees centigrade, using an excitation wavelength of 280 nm and an emission wavelength of 356 nm. The guanidine-hydrochloride concentration sufficient for 50% unfolding was found to be 3.9M for wild-type, 2.4M for BHL-1, and 0.9M for BHL-2, BHL-3, and BHL-3N. These experiments showed that BHL-1 has a higher thermodynamic stability than do the other engineered proteins, but that all of the engineered proteins have a lower thermodynamic stability than does the wild-type protein.

**Example 8 - Accessibility of the Tryptophan of BHL Proteins to Acrylamide**

Acrylamide effectively quenches the fluorescence of accessible tryptophan residues in proteins. We examined fluorescence quenching of the tryptophan residue of the BHL proteins and of the truncated WT CI-2, in the presence or absence of 6M guanidine-hydrochloride. An excitation wavelength of 295 nm was used. Emission wavelengths of 337 nm and 356 nm were used for the samples without guanidine-HCl and with guanidine-HCl, respectively. Protein concentrations of 20  $\mu$ M or 2  $\mu$ M were used for the samples without, and with guanidine-HCl, respectively. Samples were in 10 mM sodium phosphate, pH 7.0, and contained acrylamide at the following concentrations: 0, 0.0196M,

0.0385M, 0.0566M, 0.0741M, 0.0909M, 0.1071M, 0.01228M, or 0.1379M. The equation of McLure and Edelman (Biochem 6: 559-566) was used to correct for self-absorption of light by acrylamide.  $F_0/F$  was plotted against the molar acrylamide concentration, where  $F_0$  = fluorescence intensity without acrylamide, and  $F$  = fluorescence intensity with acrylamide. The slope of each line (known as the Stern-Volmer constant) was determined. The mean of 2 experiments is presented below. Values in parentheses are standard deviations.

Protein	6M guanidine-HCl	Slope
BHL-1	-	3.5 (0.3)
BHL-1	+	16.9 (1.3)
BHL-2	-	4.6 (0.4)
BHL-2	+	19.0 (0.1)
BHL-3	-	2.4 (0.2)
BHL-3	+	17.5 (0.04)
BHL-3N	-	5.8 (0.1)
BHL-3N	+	16.6 (0.6)
WT CI-2	-	1.7 (0.1)
(truncated)		
WT CI-2	+	15.7(2.1)
(truncated)		

#### 10 **Example 9 - Stabilization by Disulfide Bonds**

An examination of the WI-CI 2 three dimensional structure has identified three pairs of residues (Glu-23 and Arg-81, Thr-22 and Val-82, and VI-53 and Val-70) with an alpha carbon distance appropriate for disulfide formation. Constructs designed to substitute these residues with cysteines will be prepared.

## SEQUENCE LISTING

5

## (1) GENERAL INFORMATION

10

(i) APPLICANT: Pioneer Hi-Bred International, Inc.

(ii) TITLE OF THE INVENTION: Protein With Enhanced Levels  
of Essential Amino Acids

15

(iii) NUMBER OF SEQUENCES: 26

(iv) CORRESPONDENCE ADDRESS:

20

(A) ADDRESSEE: Pioneer Hi-Bred International, Inc.

(B) STREET: 7100 NW 62nd Avenue, P.O. Box 1000

(C) CITY: Johnston

(D) STATE: IA

(E) COUNTRY: USA

(F) ZIP: 50131

25

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette

(B) COMPUTER: IBM Compatible

(C) OPERATING SYSTEM: DOS

(D) SOFTWARE: FastSEQ for Windows Version 2.0

30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(C) CLASSIFICATION:

35

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/740,682

(B) FILING DATE: 01-NOV-1996

40

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Michel, Marianne H

(B) REGISTRATION NUMBER: 35,286

(C) REFERENCE/DOCKET NUMBER: 0571C

45

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 515-334-4467

(B) TELEFAX: 515-334-6883

(C) TELEX:

50

## (2) INFORMATION FOR SEQ ID NO:1:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...195

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

10 AAG CTG AAG ACA GAG TGG CCG GAG TTG GTG GGG AAA TCG GTG GAG AAA 48  
 Lys Leu Lys Thr Glu Trp Pro Glu Leu Val Gly Lys Ser Val Glu Lys  
 1 5 10 15

15 GCC AAG AAG GTG ATC CTG AAG GAC AAG CCA GAG GCG CAA ATC ATA GTT 96  
 Ala Lys Lys Val Ile Leu Lys Asp Lys Pro Glu Ala Gln Ile Ile Val  
 20 25 30

20 CTG CCG GTT GGT ACA AAG GTG ACG AAG GAA TAT AAG ATC GAC CGC GTC 144  
 Leu Pro Val Gly Thr Lys Val Thr Lys Glu Tyr Lys Ile Asp Arg Val  
 35 40 45

AAG CTC TTT GTG GAT AAA AAG GAC AAC ATC GCG CAG GTC CCC AGG GTC 192  
 Lys Leu Phe Val Asp Lys Lys Asp Asn Ile Ala Gln Val Pro Arg Val  
 50 55 60

25 GGC  
 195  
 Gly  
 65

30

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

45 Lys Leu Lys Thr Glu Trp Pro Glu Leu Val Gly Lys Ser Val Glu Lys  
 1 5 10 15  
 Ala Lys Lys Val Ile Leu Lys Asp Lys Pro Glu Ala Gln Ile Ile Val  
 20 25 30  
 Leu Pro Val Gly Thr Lys Val Thr Lys Glu Tyr Lys Ile Asp Arg Val  
 35 40 45

50 Lys Leu Phe Val Asp Lys Lys Asp Asn Ile Ala Gln Val Pro Arg Val  
 50 55 60  
 Gly  
 65

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: cDNA  
 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 1...195  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

AAG CTG AAG ACA GAG TGG CCG GAG TTG GTG GGG AAA TCG GTG GAG AAA      48
Lys Leu Lys Thr Glu Trp Pro Glu Leu Val Gly Lys Ser Val Glu Lys
15      1          5          10          15

GCC AAG AAG GTG ATC CTG AAG GAC AAG CCA GAG GCG CAA ATC ATA GTT      96
Ala Lys Lys Val Ile Leu Lys Asp Lys Pro Glu Ala Gln Ile Ile Val
20          20          25          30

CTA CCG GTT GGT ACA AAG GTG GCG AAG GCC TAT AAG ATC GAC AAG GTC      144
Leu Pro Val Gly Thr Lys Val Ala Lys Ala Tyr Lys Ile Asp Lys Val
35          40          45

AAG CTT TTT GTG GAT AAA AAG GAC AAC ATC GCG CAG GTC CCC AGG GTC      192
Lys Leu Phe Val Asp Lys Lys Asp Asn Ile Ala Gln Val Pro Arg Val
50          55          60

GGC
30 195
    Gly
    65
  
```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 65 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Lys Leu Lys Thr Glu Trp Pro Glu Leu Val Gly Lys Ser Val Glu Lys
1          5          10          15
Ala Lys Lys Val Ile Leu Lys Asp Lys Pro Glu Ala Gln Ile Ile Val
50      20          25          30
Leu Pro Val Gly Thr Lys Val Ala Lys Ala Tyr Lys Ile Asp Lys Val
35          40          45
Lys Leu Phe Val Asp Lys Lys Asp Asn Ile Ala Gln Val Pro Arg Val
55      50          55          60
    Gly
    65
  
```

(2) INFORMATION FOR SEQ ID NO:5:



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence

- (B) LOCATION: 1...195

- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AAG CTG AAG ACA GAG TGG CCG GAG TTG GTG GGG AAA TCG GTG GAG AAA 48  
 Lys Leu Lys Thr Glu Trp Pro Glu Leu Val Gly Lys Ser Val Glu Lys  
 1 5 10 15

GCC AAG AAG GTG ATC CTG AAG GAC AAG CCA GAG GCG CAA ATC ATA GTT 96  
 Ala Lys Lys Val Ile Leu Lys Asp Lys Pro Glu Ala Gln Ile Ile Val  
 20 25 30

CTA CCG GTT GGT ACA AAG GTG GGT AAG CAT TAT AAG ATC GAC AAG GTC 144  
 Leu Pro Val Gly Thr Lys Val Gly Lys His Tyr Lys Ile Asp Lys Val  
 35 40 45

AAG CTT TTT GTG GAT AAA AAG GAC AAC ATC GCG CAG GTC CCC AGG GTC 192  
 Lys Leu Phe Val Asp Lys Lys Asp Asn Ile Ala Gln Val Pro Arg Val  
 50 55 60

GGC

195

Gly

65

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Lys Leu Lys Thr Glu Trp Pro Glu Leu Val Gly Lys Ser Val Glu Lys  
 1 5 10 15

Ala Lys Lys Val Ile Leu Lys Asp Lys Pro Glu Ala Gln Ile Ile Val  
 20 25 30

Leu Pro Val Gly Thr Lys Val Gly Lys His Tyr Lys Ile Asp Lys Val  
 35 40 45

Lys Leu Phe Val Asp Lys Lys Asp Asn Ile Ala Gln Val Pro Arg Val  
 50 55 60

Gly

65

## (2) INFORMATION FOR SEQ ID NO:7:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 249 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 10 (ii) MOLECULE TYPE: cDNA  
 (ix) FEATURE:  
 (A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 1...249  
 15 (D) OTHER INFORMATION:  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

20 AAG TCG GTG GAG AAG AAA CCG AAG GGT GTG AAG ACA GGT GCG GGT GAC 48  
 Lys Ser Val Glu Lys Lys Pro Lys Gly Val Lys Thr Gly Ala Gly Asp  
 1 5 10 15

25 AAG CAT AAG CTG AAG ACA GAG TGG CCG GAG TTG GTG GGG AAA TCG GTG 96  
 Lys His Lys Leu Lys Thr Glu Trp Pro Glu Leu Val Gly Lys Ser Val  
 20 25 30

30 GAG AAA GCC AAG AAG GTG ATC CTG AAG GAC AAG CCA GAG GCG CAA ATC 144  
 Glu Lys Ala Lys Lys Val Ile Leu Lys Asp Lys Pro Glu Ala Gln Ile  
 35 40 45

35 ATA GTT CTA CCG GTT GGT ACA AAG GTG GGT AAG CAT TAT AAG ATC GAC 192  
 Ile Val Leu Pro Val Gly Thr Lys Val Gly Lys His Tyr Lys Ile Asp  
 50 55 60

40 AAG GTC AAG CTT TTT GTG GAT AAA AAG GAC AAC ATC GCG CAG GTC CCC 240  
 Lys Val Lys Leu Phe Val Asp Lys Lys Asp Asn Ile Ala Gln Val Pro  
 65 70 75 80

40 AGG GTC GGC  
 249  
 Arg Val Gly

## 45 (2) INFORMATION FOR SEQ ID NO:8:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 83 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (v) FRAGMENT TYPE: internal  
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Lys Ser Val Glu Lys Lys Pro Lys Gly Val Lys Thr Gly Ala Gly Asp  
 1 5 10 15

Lys His Lys Leu Lys Thr Glu Trp Pro Glu Leu Val Gly Lys Ser Val  
 20 25 30  
 Glu Lys Ala Lys Lys Val Ile Leu Lys Asp Lys Pro Glu Ala Gln Ile  
 35 40 45  
 5 Ile Val Leu Pro Val Gly Thr Lys Val Gly Lys His Tyr Lys Ile Asp  
 50 55 60  
 Lys Val Lys Leu Phe Val Asp Lys Lys Asp Asn Ile Ala Gln Val Pro  
 65 70 75 80  
 Arg Val Gly

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 1...249  
 (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AAG TCG GTG GAG AAG AAA CCG AAG GGT GTG AAG ACA GGT GCG GGT GAC 48  
 Lys Ser Val Glu Lys Lys Pro Lys Gly Val Lys Thr Gly Ala Gly Asp  
 1 5 10 15  
 AAG CAT AAG CTG AAG ACA GAG TGG CCG GAG TTG GTG GGG AAA TCG GTG 96  
 Lys His Lys Leu Lys Thr Glu Trp Pro Glu Leu Val Gly Lys Ser Val  
 20 25 30  
 GAG AAA GCC AAG AAG GTG ATC CTG AAG GAC AAG CCA GAG GCG CAA ATC 144  
 Glu Lys Ala Lys Lys Val Ile Leu Lys Asp Lys Pro Glu Ala Gln Ile  
 35 40 45  
 ATA GTT CTA CCG GTT GGT ACA AAG GTG ACG AAG GAA TAT AAG ATC GAC 192  
 Ile Val Leu Pro Val Gly Thr Lys Val Thr Lys Glu Tyr Lys Ile Asp  
 50 55 60  
 CGC GTC AAG CTT TTT GTG GAT AAA AAG GAC AAC ATC GCG CAG GTC CCC 240  
 Arg Val Lys Leu Phe Val Asp Lys Lys Asp Asn Ile Ala Gln Val Pro  
 65 70 75 80  
 AGG GTC GGC  
 249  
 Arg Val Gly

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids  
 (B) TYPE: amino acid

(C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (v) FRAGMENT TYPE: internal

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Lys Ser Val Glu Lys Lys Pro Lys Gly Val Lys Thr Gly Ala Gly Asp  
 1 5 10 15  
 10 Lys His Lys Leu Lys Thr Glu Trp Pro Glu Leu Val Gly Lys Ser Val  
 20 25 30  
 Glu Lys Ala Lys Lys Val Ile Leu Lys Asp Lys Pro Glu Ala Gln Ile  
 35 40 45  
 15 Ile Val Leu Pro Val Gly Thr Lys Val Thr Lys Glu Tyr Lys Ile Asp  
 50 55 60  
 Arg Val Lys Leu Phe Val Asp Lys Lys Asp Asn Ile Ala Gln Val Pro  
 65 70 75 80  
 Arg Val Gly

20

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 249 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

30

(A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 1...249  
 (D) OTHER INFORMATION:

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AAG TCG GTG GAG AAG AAA CCG AAG GGT GTG AAG ACA GGT GCG GGT GAC 48  
 Lys Ser Val Glu Lys Lys Pro Lys Gly Val Lys Thr Gly Ala Gly Asp  
 1 5 10 15  
 40 AAG CAT AAG CTG AAG ACA GAG TGG CCG GAG TTG GTG GGG AAA TCG GTG 96  
 Lys His Lys Leu Lys Thr Glu Trp Pro Glu Leu Val Gly Lys Ser Val  
 20 25 30  
 45 GAG AAA GCC AAG AAG GTG ATC CTG AAG GAC AAG CCA GAG GCG CAA ATC 144  
 Glu Lys Ala Lys Lys Val Ile Leu Lys Asp Lys Pro Glu Ala Gln Ile  
 35 40 45  
 50 ATA GTT CTA CCG GTT GGT ACA AAG GTG GCG AAG GCC TAT AAG ATC GAC 192  
 Ile Val Leu Pro Val Gly Thr Lys Val Ala Lys Ala Tyr Lys Ile Asp  
 50 55 60  
 55 AAG GTC AAG CTT TTT GTG GAT AAA AAG GAC AAC ATC GCG CAG GTC CCC 240  
 Lys Val Lys Leu Phe Val Asp Lys Lys Asp Asn Ile Ala Gln Val Pro  
 65 70 75 80

AGG GTC GGC

249

Arg Val Gly

5 (2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 83 amino acids

(B) TYPE: amino acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```

Lys Ser Val Glu Lys Lys Pro Lys Gly Val Lys Thr Gly Ala Gly Asp
 1             5             10             15
Lys His Lys Leu Lys Thr Glu Trp Pro Glu Leu Val Gly Lys Ser Val
20             20             25             30
Glu Lys Ala Lys Lys Val Ile Leu Lys Asp Lys Pro Glu Ala Gln Ile
35             40             45
Ile Val Leu Pro Val Gly Thr Lys Val Ala Lys Ala Tyr Lys Ile Asp
50             55             60
25 Lys Val Lys Leu Phe Val Asp Lys Lys Asp Asn Ile Ala Gln Val Pro
65             70             75             80
Arg Val Gly

```

30 (2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 base pairs

(B) TYPE: nucleic acid

35 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

40 (A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...249

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

45 AGT TCA GTG GAG AAG AAG CCG GAG GGA GTG AAC ACC GGT GCT GGT GAC      48
   Ser Ser Val Glu Lys Lys Pro Glu Gly Val Asn Thr Gly Ala Gly Asp
   1             5             10             15

50 CGT CAC AAC CTG AAG ACA GAG TGG CCA GAG TTG GTG GGG AAA TCG GTG      96
   Arg His Asn Leu Lys Thr Glu Trp Pro Glu Leu Val Gly Lys Ser Val
           20             25             30

55 GAG GAG GCC AAG AAG GTG ATT CTG CAG GAC AAG CCA GAG GCG CAA ATC      144
   Glu Glu Ala Lys Lys Val Ile Leu Gln Asp Lys Pro Glu Ala Gln Ile
           35             40             45

ATA GTT CTA CCG GTG GGG ACA ATT GTG ACC ATG GAA TAT CGG ATC GAC      192

```

Ile Val Leu Pro Val Gly Thr Ile Val Thr Met Glu Tyr Arg Ile Asp  
 50 55 60

5 CGC GTC CGC CTC TTT GTC GAT AAA CTC GAC AAC ATT GCC CAG GTC CCC 240  
 Arg Val Arg Leu Phe Val Asp Lys Leu Asp Asn Ile Ala Gln Val Pro  
 65 70 75 80

AGG GTC GGC  
 249  
 10 Arg Val Gly

(2) INFORMATION FOR SEQ ID NO:14:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

25

Ser Ser Val Glu Lys Lys Pro Glu Gly Val Asn Thr Gly Ala Gly Asp  
 1 5 10 15  
 Arg His Asn Leu Lys Thr Glu Trp Pro Glu Leu Val Gly Lys Ser Val  
 20 25 30  
 30 Glu Glu Ala Lys Lys Val Ile Leu Gln Asp Lys Pro Glu Ala Gln Ile  
 35 40 45  
 Ile Val Leu Pro Val Gly Thr Ile Val Thr Met Glu Tyr Arg Ile Asp  
 50 55 60  
 Arg Val Arg Leu Phe Val Asp Lys Leu Asp Asn Ile Ala Gln Val Pro  
 35 65 70 75 80  
 Arg Val Gly

(2) INFORMATION FOR SEQ ID NO:15:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 45 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

50

- (A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 1...288  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

55 GCA GTG CAA CAA GCA AGA TTT ACC TGC CCA TCG ATC ATA TCG TCA ACT 48  
 Ala Val Gln Gln Ala Arg Phe Thr Cys Pro Ser Ile Ile Ser Ser Thr  
 1 5 10 15

GGT CCG GCA GTT CGC GAC ACC ATG AGC TCC ACG GAG TGC GGC GGC GGC 96  
 Gly Pro Ala Val Arg Asp Thr Met Ser Ser Thr Glu Cys Gly Gly Gly  
 20 25 30

5 GGC GGC GGC GCC AAG ACG TCG TGG CCT GAG GTG GTC GGG CTG AGC GTG 144  
 Gly Gly Gly Ala Lys Thr Ser Trp Pro Glu Val Val Gly Leu Ser Val  
 35 40 45

10 GAG GAC GCC AAG AAG GTG ATG GTC AAG GAC AAG CCG GAC GCC GAC ATC 192  
 Glu Asp Ala Lys Lys Val Met Val Lys Asp Lys Pro Asp Ala Asp Ile  
 50 55 60

15 GTG GTG CTG CCC GTC GGC TCC GTG GTG ACC GCG GAT TAT CGC CCT AAC 240  
 Val Val Leu Pro Val Gly Ser Val Val Thr Ala Asp Tyr Arg Pro Asn  
 65 70 75 80

20 CGT GTC CGC ATC TTC GTC GAC ATC GTC GCC CAG ACG CCC CAC ATC GGC T 289  
 Arg Val Arg Ile Phe Val Asp Ile Val Ala Gln Thr Pro His Ile Gly  
 85 90 95

GATAATATAT AAGCTAGCCG CTATTTTCCTT TCCTTGCCCC AGAACTTGAA ATAAATATAT  
 349  
 ATACGATGAA ATAACGCGGG CATGCCGAAT A-ATGGA-TG TG--TGAATT CTCACTAATT  
 409

25 AAGTAATG-C ATAAATAAAC GTATTCAAAA AAAAAAAAAA AAAAAAAAAA  
 459

## (2) INFORMATION FOR SEQ ID NO:16:

## 30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## 35 (ii) MOLECULE TYPE: protein

- (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

40 Ala Val Gln Gln Ala Arg Phe Thr Cys Pro Ser Ile Ile Ser Ser Thr  
 1 5 10 15  
 Gly Pro Ala Val Arg Asp Thr Met Ser Ser Thr Glu Cys Gly Gly Gly  
 20 25 30  
 Gly Gly Gly Ala Lys Thr Ser Trp Pro Glu Val Val Gly Leu Ser Val  
 35 40 45  
 Glu Asp Ala Lys Lys Val Met Val Lys Asp Lys Pro Asp Ala Asp Ile  
 50 55 60  
 Val Val Leu Pro Val Gly Ser Val Val Thr Ala Asp Tyr Arg Pro Asn  
 65 70 75 80  
 50 Arg Val Arg Ile Phe Val Asp Ile Val Ala Gln Thr Pro His Ile Gly  
 85 90 95

## (2) INFORMATION FOR SEQ ID NO:17:

## 55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(ix) FEATURE:

5 (A) NAME/KEY: Coding Sequence  
(B) LOCATION: 1...303  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

10 CGA CCC ACG CGT CCG CCC ACG CGT CCG GCA AGA TTT ACC TGC CCA TCG 48  
Arg Pro Thr Arg Pro Pro Thr Arg Pro Ala Arg Phe Thr Cys Pro Ser  
1 5 10 15

15 ATC ATA TCG TCA ACT GGT CCG GCA GTT CGC GAC ACC ATG AGC TCC ACG 96  
Ile Ile Ser Ser Thr Gly Pro Ala Val Arg Asp Thr Met Ser Ser Thr  
20 25 30

20 GAG TGC GGC GGC GGC GGC GGC GGC GCC AAG ACG TCG TGG CCT GAG GTG 144  
Glu Cys Gly Gly Gly Gly Gly Gly Ala Lys Thr Ser Trp Pro Glu Val  
35 40 45

25 GTC GGG CTG AGC GTG GAG GAC GCC AAG AAG GTG ATC CTC AAG GAC AAG 192  
Val Gly Leu Ser Val Glu Asp Ala Lys Lys Val Ile Leu Lys Asp Lys  
50 55 60

30 CCG GAC GCC GAC ATC GTG GTG CTG CCC GTC GGC TCC GTG GTG ACC GCG 240  
Pro Asp Ala Asp Ile Val Val Leu Pro Val Gly Ser Val Val Thr Ala  
65 70 75 80

35 GAT TAT CGC CCT AAC CGT GTC CGC ATC TTC GTC GAC ATC GTC GCC CAG 288  
Asp Tyr Arg Pro Asn Arg Val Arg Ile Phe Val Asp Ile Val Ala Gln  
85 90 95

40 ACG CCC CAC ATC GGC TGATAATATA TAAGCTAGCC GCTATTTTCCT TTCCTTGCCC C 344  
Thr Pro His Ile Gly  
100

40 AGAACTTGAA ATAAATATAT ATACGATGAA ATAACGCGGG CATGCCGAAT AATGGATGTG 404  
TGAAAAAAAA AAAAAAAAAA AAAA  
428

(2) INFORMATION FOR SEQ ID NO:18:

45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 101 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
50 (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: protein  
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

55 Arg Pro Thr Arg Pro Pro Thr Arg Pro Ala Arg Phe Thr Cys Pro Ser  
1 5 10 15  
Ile Ile Ser Ser Thr Gly Pro Ala Val Arg Asp Thr Met Ser Ser Thr



20 25 30  
 Glu Cys Gly Gly Gly Gly Gly Gly Ala Lys Thr Ser Trp Pro Glu Val  
 35 40 45  
 Val Gly Leu Ser Val Glu Asp Ala Lys Lys Val Ile Leu Lys Asp Lys  
 5 50 55 60  
 Pro Asp Ala Asp Ile Val Val Leu Pro Val Gly Ser Val Val Thr Ala  
 65 70 75 80  
 Asp Tyr Arg Pro Asn Arg Val Arg Ile Phe Val Asp Ile Val Ala Gln  
 85 90 95  
 10 Thr Pro His Ile Gly  
 100

## (2) INFORMATION FOR SEQ ID NO:19:

- 15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 441 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 20 (ii) MOLECULE TYPE: cDNA  
 (ix) FEATURE:  
 (A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 1...255  
 25 (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

30 TTA ATT ATT GCC CTT TCA GTT NGC CAT CGG CAG CCG AGC ACC ATG AGC 48  
 Leu Ile Ile Ala Leu Ser Val Xaa His Arg Gln Pro Ser Thr Met Ser  
 1 5 10 15  
 TCC ACA GGC GGC GGC GAC GAT GGC GCC AAG AAG TCT TGG CCG GAA GTG 96  
 Ser Thr Gly Gly Gly Asp Asp Gly Ala Lys Lys Ser Trp Pro Glu Val  
 35 20 25 30  
 GTC GGG CTC AGC CTG GAA GAA GCC AAG AGG GTG ATC CTG TGC GAC AAG 144  
 Val Gly Leu Ser Leu Glu Glu Ala Lys Arg Val Ile Leu Cys Asp Lys  
 40 35 40 45  
 CCC GAC GCC GAC ATC GTC GTG CTG CCC GTC GGC ACG CCG GTG ACC ATG 192  
 Pro Asp Ala Asp Ile Val Val Leu Pro Val Gly Thr Pro Val Thr Met  
 50 50 55 60  
 GAT TTC CGC CCC AAC CGC GTC CGC ATC TTC GTC GAC ACC GTC GCG GAG 240  
 Asp Phe Arg Pro Asn Arg Val Arg Ile Phe Val Asp Thr Val Ala Glu  
 65 70 75 80  
 GCA MCC CAC ATC GGC TGAGGTTAAA TCTACAAAAT GAATGAYTCG GACATGCCAT G 296  
 50 Ala Xaa His Ile Gly  
 85  
 CGTAC-TGTC CGTCGCCGAA TAATGGATGT GTGTGTGCTT CGATCGTTCC TAATAAGTTG  
 356  
 55 CTAGT-AAAA ATAAT-GGCA TCGTCGTTA- TGCATGAATA AAAAGTATCA GAATAATGTT  
 416  
 CACCCTTTC- AAAAAAAAAA AAAAA  
 441

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

Leu Ile Ile Ala Leu Ser Val Xaa His Arg Gln Pro Ser Thr Met Ser
1           5           10           15
Ser Thr Gly Gly Gly Asp Asp Gly Ala Lys Lys Ser Trp Pro Glu Val
          20           25           30
Val Gly Leu Ser Leu Glu Glu Ala Lys Arg Val Ile Leu Cys Asp Lys
          35           40           45
Pro Asp Ala Asp Ile Val Val Leu Pro Val Gly Thr Pro Val Thr Met
          50           55           60
Asp Phe Arg Pro Asn Arg Val Arg Ile Phe Val Asp Thr Val Ala Glu
65           70           75           80
Ala Xaa His Ile Gly
          85

```

## (2) INFORMATION FOR SEQ ID NO:21:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 1...213  
 (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```

GTG CGT CGT CGG CGA ACA GCC ACC GGC GGC AAG ACG TCG TGG CCG GAG      48
Val Arg Arg Arg Arg Thr Ala Thr Gly Gly Lys Thr Ser Trp Pro Glu
45 1           5           10           15

GTG GTC GGG CTG AGC GTC GAG GAA GCC AAG AAG GTG ATT CTG GCG GAC      96
Val Val Gly Leu Ser Val Glu Glu Ala Lys Lys Val Ile Leu Ala Asp
          20           25           30

AAG CCG AAC GCC GAC ATC GTG GTG CTG CCC ACC ACC ACG CAG GCG GTG      144
Lys Pro Asn Ala Asp Ile Val Val Leu Pro Thr Thr Thr Gln Ala Val
          35           40           45

ACC TCC GAC TTT GGG TTC GAC CGT GTC CGC GTC TTC GTC GGG ACC GTC      192
Thr Ser Asp Phe Gly Phe Asp Arg Val Arg Val Phe Val Gly Thr Val
          50           55           60

```

GCC CAG ACG CCC CAT GTT GGC TAGGCTAGAG CCTCAGCCTA GAGGTCGTCG GCAC 247  
 Ala Gln Thr Pro His Val Gly  
 65 70

5 CGCCGGCCAT GACCACCTGC TA-TATGTCA CT-ACTAGTA ATAAAGTATW AATAACAGGG  
 307  
 AGGATGCATG CTCATC-TTG GAATCTGTAC GCTTGTTGGA CTACTACTTG GCTACTTGAA  
 367  
 AAAAAAAAAA AAAAA  
 10 382

(2) INFORMATION FOR SEQ ID NO:22:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 71 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 20 (ii) MOLECULE TYPE: protein  
 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

25 Val Arg Arg Arg Arg Thr Ala Thr Gly Gly Lys Thr Ser Trp Pro Glu  
 1 5 10 15  
 Val Val Gly Leu Ser Val Glu Glu Ala Lys Lys Val Ile Leu Ala Asp  
 20 25 30  
 Lys Pro Asn Ala Asp Ile Val Val Leu Pro Thr Thr Thr Gln Ala Val  
 35 40 45  
 30 Thr Ser Asp Phe Gly Phe Asp Arg Val Arg Val Phe Val Gly Thr Val  
 50 55 60  
 Ala Gln Thr Pro His Val Gly  
 65 70

35 (2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 448 base pairs  
 40 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: cDNA  
 (ix) FEATURE:  
 45 (A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 1...240  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

50 CGA TTT AGC TAT AGC AGG TCT CGA TCG GCG GCC ATG AGC GGT AGC CGC 48  
 Arg Phe Ser Tyr Ser Arg Ser Arg Ser Ala Ala Met Ser Gly Ser Arg  
 1 5 10 15  
 55 AGC AAG AAG TCG TGG CCG GAG GTG GAG GGG CTG CCG TCC GAG GTG GCC 96  
 Ser Lys Lys Ser Trp Pro Glu Val Glu Gly Leu Pro Ser Glu Val Ala  
 20 25 30

AAG CAG AAA ATT CTG GCC GAC CGC CCG GAC GTC CAG GTG GTC GTT CTG 144  
 Lys Gln Lys Ile Leu Ala Asp Arg Pro Asp Val Gln Val Val Val Leu  
 35 40 45  
 5 CCC GAC GGC TCC TTC GTC ACC ACT GAT TTC AAC GAC AAG CGC GTC CGG 192  
 Pro Asp Gly Ser Phe Val Thr Thr Asp Phe Asn Asp Lys Arg Val Arg  
 50 55 60  
 10 GTC TTC GTC GAC AAC GCC GAC AAC GTC GCC AAA GTC CCC AAG ATC GGC T 241  
 Val Phe Val Asp Asn Ala Asp Asn Val Ala Lys Val Pro Lys Ile Gly  
 65 70 75 80  
 AGCTAGCTAG CTAGGCCCAA TCGTTCTAAT CAGCTAGTTT CTTTCTTTCA TAAATAAAAG  
 301  
 15 TCCTCTCTCG TACCCGGACT GTGATGTTTC CCTAGTTGTC TCGTACGTGT TGTTTTCTGT  
 361  
 CTTAATGGAT GCCATGGCGC CCGCGCGCGC CTYCATCATG AAAAGCTACA TTTGAAACGA  
 421  
 TTTT-AGTAT TCTTTGCTGT TAAAAAA  
 20 448

## (2) INFORMATION FOR SEQ ID NO:24:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 80 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 30 (ii) MOLECULE TYPE: protein  
 (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

35 Arg Phe Ser Tyr Ser Arg Ser Arg Ser Ala Ala Met Ser Gly Ser Arg  
 1 5 10 15  
 Ser Lys Lys Ser Trp Pro Glu Val Glu Gly Leu Pro Ser Glu Val Ala  
 20 25 30  
 Lys Gln Lys Ile Leu Ala Asp Arg Pro Asp Val Gln Val Val Val Leu  
 35 40 45  
 40 Pro Asp Gly Ser Phe Val Thr Thr Asp Phe Asn Asp Lys Arg Val Arg  
 50 55 60  
 Val Phe Val Asp Asn Ala Asp Asn Val Ala Lys Val Pro Lys Ile Gly  
 65 70 75 80

45 (2) INFORMATION FOR SEQ ID NO:25:

50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 18 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

55 ATGAAGTCGG TGGAGAAG

18

## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GCCGACCCTG GGGACCTG

18

All publications and patent applications mentioned in this specification are indicative of the level of skill of those skilled in the art to which this invention pertains. All publications and patent applications are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and  
5 individually indicated to be incorporated by reference.

Variations on the above embodiments are within the ability of one of ordinary skill in the art, and such variations do not depart from the scope of the present invention as described in the following claims.

We Claim:

1. A polypeptide comprising at least 10 contiguous amino acid residues from a protein having Seq. ID No. 2, 4, 6, 8, 10, 12, 16, 18, 20, 22, or 24:

5 wherein the polypeptide, when presented to an interacting molecule, specifically binds to the molecule;

wherein the interacting molecule is also capable of binding to the protein;

wherein the polypeptide does not bind to the interacting molecule, which has been fully absorbed with the protein; and

10 wherein the polypeptide has at least one more essential amino acid than the non-modified polypeptide.

2. The polypeptide of claim 1 comprising at least 20 contiguous amino acid residues.

3. The polypeptide of claim 2 comprising at least 30 contiguous amino acid residues.

15 4. The polypeptide of claim 1 comprising Seq. ID No. 2, 4, 6, 8, 10, 12, 16, 18, 20, 22, or 24.

5. The polypeptide of claim 4 having Seq. ID No. 2, 4, 6, 8, 10, 12, 16, 18, 20, 22, or 24.

20 6. The polypeptide of claim 1 which contains or is modified to contain essential amino acids at positions 1, 8, 11, 17, 19, 34, 41, 56, 59, 62, 65, 67 or 73 in SEQ ID Nos. 8, 10, 12, 16, 18, 20, 22, or 24 or at positions 1, 16, 23, 41, 44, 49 or 55 in SEQ ID Nos. 2, 4 and 6.

7. The polypeptide of claim 1 which contains or is modified to contain non-wild type amino acid residues at positions from about 53 to about 70.

25 8. The polypeptide of claim 7 wherein non-wild type amino acid residues are located at positions 58-60, 62, 65, or 67.

9. The polypeptide of claim 8 wherein the non-wild type amino acid residue is located at position 59.
10. The polypeptide of claim 6 wherein the essential amino acid is lysine, tryptophan, methionine, threonine or mixtures thereof.
- 5 11. The polypeptide of claim 1, wherein the interactive molecule is an antibody elicited when the polypeptide is presented as an immunogen.
12. The polypeptide of claim 1 which is about 7.3 Kda or about 9.2 Kda.
13. The polypeptide of claim 1 further comprising more than one or less than 50 additional amino terminal amino acid residues.
- 10 14. The polypeptide of claim 13 wherein one of the amino terminal amino acid residues is methionine.
15. The polypeptide of claim 13 wherein the additional amino terminal amino acids are essential amino acids.
16. The polypeptide of claim 1 which is a cleavage product.
- 15 17. The polypeptide of claim 1 which is recombinantly produced.
18. The polypeptide comprising Seq. ID No. 2, 4, 6, 8,10, 12, 16, 18, 20,22, or 24.
19. A nucleic acid encoding the polypeptide of Claim 1.
20. A nucleic acid encoding the polypeptide of claim 4.
21. The nucleic acid of claim 19 which is DNA.
- 20 22. A nucleic acid encoding the polypeptide of claim 18.
23. A second nucleic acid which is complementary to the nucleic acid of claim 19.
24. A recombinant expression cassette comprising the nucleic acid of claim 19, operably linked to a promoter.



25. The recombinant expression cassette of Claim 22, wherein the promoter provides for protein expression in plants.
26. The recombinant expression cassette of Claim 22, wherein the promoter provides for protein expression in bacteria, yeast or virus.
- 5 27. Transformed plant cells containing the recombinant expression cassette of Claim 24.
28. A transformed plant containing at least one copy of the recombinant expression cassette of Claim 24.
29. A seed of the transformed plant of claim 28.
- 10 30. A polypeptide produced by substituting an essential amino acid for at least one but less than all of the amino acid residues in a protease inhibitor for enhancing the nutritional value of feed wherein the polypeptide exhibits reduced inhibitory activity compared to the wild type protein.
- 15 31. The polypeptide of claim 30, wherein more than about 55% but less than about 95% of the amino acid residues are essential amino acids.
32. The polypeptide of claim 31, wherein more than about 55% but less than about 90% of the amino acid residues are essential amino acids.
33. The polypeptide of claim 32, wherein more than about 55% but less than about 85% of the amino acid residues are essential amino acids.
- 20 34. The polypeptide of claim 30, wherein hydrogen bonding is disrupted in the active loop of the protease inhibitor.
35. The polypeptide of claim 34, which exhibits decreased protease inhibitor activity as compared to the wild-type protein.
- 25 36. The polypeptide of claim 30 which exhibits less than about 30% of the protease inhibitor activity compared to corresponding wild-type protein which does not have substituted amino acid residues.

37. The polypeptide of claim 30 wherein the essential amino acid is lysine, tryptophan, methionine, threonine or mixtures thereof.

38. The polypeptide of claim 37, wherein the protease inhibitor protein is derived from a plant.

5 39. The polypeptide of Claim 37, wherein the protease inhibitor protein is a chymotrypsin inhibitor-like polypeptide.

40. A nucleic acid comprising a member selected from the group consisting of:

(a) a polynucleotide having at least 60% identity to a polynucleotide encoding a polypeptide selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 16, 18, 20, 22, 24 and 26 wherein said polypeptide when presented as an immunogen elicits the production of an antibody which is specifically reactive to said polypeptide;

(b) a polynucleotide which is complementary to said polynucleotide of (a);  
and

(c) a polynucleotide comprising at least 30 contiguous nucleotides from a polynucleotide of (a) or (b).

41. A protein comprising a polypeptide of at least 10 contiguous amino acids encoded by the isolated nucleic acid of claim 40.

42. The protein of claim 40, wherein said polypeptide has a sequence selected from the group consisting of SEQ ID NOS:2, 4, 6, 8, 10, 12, 16, 18, 20, 22, 24 or 26.

43. A nucleic acid comprising a polynucleotide of at least 30 nucleotides in length which selectively hybridizes under stringent conditions to a nucleic acid selected from the group consisting of SEQ ID NOS:1,3,5,7,9,11,15,17,19,21,23, 25 or a complement thereof.

44. A nucleic acid selected from the group Seq. ID No. 1,3,5,7,9,11,15,17,19,21, or 23.

45. A nucleic acid comprising at least 10 contiguous nucleotides selected from the group consisting of 1,3,5,7,9,11,15,17,19,21 and 23.

46. A nucleic acid comprising the sequence of SEQ ID No. 1, 3, 5,7,9,11,15,17,19,21, or 23 or a nucleic acid having at least 70% identity thereto, wherein the nucleic acid

encodes for a polypeptide which exhibits reduced protease inhibitor activity compared to a corresponding wild-type protein.

47. The nucleic acid of Claim 37 which exhibits 80% identity.

48. The nucleic acid of Claim 38 which exhibits 90% identity.

5 49. A second nucleic acid which is complementary to the nucleic acid of Claim 37.

50. The nucleic acid of Claim 49 which is DNA.

51. A nucleic acid encoding a protease inhibitor protein wherein nucleotides have been substituted to increase the number of essential amino acids in the encoded protein.

52. The nucleic acid of Claim 51 wherein the inhibitor protein is derived from a plant.

10 53. The nucleic acid of Claim 52 wherein the inhibitor protein is a protease inhibitor polypeptide.

54. A nucleic acid encoding the polypeptide of claim 51.

55. An isolated nucleic acid comprising a polynucleotide having a sequence of a nucleic acid amplified from a plant nucleic acid library using the primers selected from  
15 the group consisting of: Seq. ID No. 25 and 26, or complements thereof.

56. An isolated nucleic acid comprising a polynucleotide encoding a polypeptide wherein:

(a) said polypeptide comprises at least 10 contiguous amino acid residues from a first polypeptide selected from the group consisting of SEQ ID  
20 NOS: 2, 4, 6, 8, 10, 12, 16, 18, 20, 22, and 24, and wherein said polypeptide, when presented as an immunogen, elicits the production of an antibody which specifically binds to said first polypeptide;

(b) said polypeptide does not bind to antisera raised against said first polypeptide which has been fully immunosorbed with said first  
25 polypeptide;

(c) said polypeptide has a molecular weight in non-glycosylated form within 10% of said first polypeptide.

57. A heterologous promoter operably linked to a non-isolated protease inhibitor polynucleotide encoding a polypeptide encoded by the nucleic acid of claim 56.

30 58. An recombinant expression cassette comprising the nucleic acid comprising a nucleic acid of Claim 46, operably linked to a promoter.

59. The recombinant expression cassette of Claim 58, wherein promoter provides for protein expression in plants.
60. The expression cassette of Claim 58, wherein the promoter provides for protein expression in bacteria, yeast or virus.
- 5 61. Transformed plant cells containing the recombinant expression cassette of Claim 58.
62. A transformed plant containing at least one copy of the expression cassette of Claim 58.
63. The plant of Claim 59 which is a monocotyledonous plant.
- 10 64. The plant of Claim 63 which is selected from the group consisting of maize, sorghum, wheat, rice and barley.
65. The transformed plant of Claim 59 which is a dicotyledonous plant.
66. The plant of Claim 65 which is selected from the group consisting of soybean, alfalfa, canola, sunflower, tobacco, tomato and canola.
- 15 67. The transformed plant of Claim 59 which is maize or soybeans.
68. A transformed plant containing the isolated polypeptide of Claim 1.
69. A seed produced by the transformed plant of Claim 68.
70. An animal feed composition comprising the polypeptide of Claim 62.
71. An animal feed composition comprising the plant of Claim 38.
- 20 72. An animal feed composition comprising the seed of Claim 69.
73. A method for increasing the nutritional value of a plant comprising introducing into the cells of the plant the expression cassette of Claim 58 to yield transformed plant cells; and regenerating a transformed plant from the transformed plant cells.
74. The method of claim 73, wherein the transformed plant is maize.

75. The isolated nucleic acid comprising a polynucleotide which is the product of PCR amplification from *Zea mays* with primers having the of Seq. ID No 25 and 26.

76. An isolated polypeptide comprising at least 10 contiguous amino acid residues from a protein having Seq. ID No. 2, 4, 6, 8, 10, 12, 16, 18, 20, 22, or 24:

5            wherein the polypeptide, when presented to an interacting molecule, specifically binds to the molecule;

             wherein the interacting molecule is also capable of binding to the protein;

             wherein the polypeptide does not bind to the interacting molecule, which has been fully absorbed with the protein; and

10           wherein the polypeptide and has at least one more essential amino acid than the non-modified polypeptide.

77. The isolated polypeptide of claim 76 comprising at least 20 contiguous amino acid residues.

15           78. The isolated polypeptide of claim 77 comprising at least 30 contiguous amino acid residues.

79. The isolated polypeptide of claim 76 comprising Seq. ID No. 2, 4, 6, 8, 10, 12, 16, 18, 20, 22, or 24.

80. The isolated polypeptide of claim 79 having Seq. ID No. 2, 4, 6, 8, 10, 12, 16, 18, 20, 22, or 24.

20           81. The isolated polypeptide of claim 76 which contains or is modified to contain essential amino acids at positions 1, 8, 11, 17, 19, 34, 41, 56, 59, 62, 65, 67 or 73 in SEQ ID Nos. 8, 10, 12, 16, 18, 20, 22, or 24 or at positions 1, 16, 23, 41, 44, 49 or 55 in SEQ ID Nos. 2, 4 and 6.

25           82. The isolated polypeptide of claim 76 which contains or is modified to contain non-wild type amino acid residues at positions from about 53 to about 70.

83. The isolated polypeptide of claim 82 wherein non-wild type amino acid residues are located at positions 58-60, 62, 65, or 67.
84. The isolated polypeptide of claim 83 wherein the non-wild type amino acid residue is located at position 59.
- 5 85. The isolated polypeptide of claim 81 wherein the essential amino acid is lysine, tryptophan, methionine, threonine or mixtures thereof.
86. The isolated polypeptide of claim 76, wherein the interactive molecule is an antibody elicited when the polypeptide is presented as an immunogen.
87. The isolated polypeptide of claim 76 which is about 7.3 Kda or about 9.2 Kd.
- 10 88. The isolated polypeptide of claim 76 further comprising more than one or less than 50 additional amino terminal amino acid residues.
89. The isolated polypeptide of claim 88 wherein one of the amino terminal amino acid residues is methionine.
- 15 90. The isolated polypeptide of claim 88 wherein the additional amino terminal amino acids are essential amino acids.
91. The isolated polypeptide of claim 76 which is a cleavage product.
92. The isolated polypeptide of claim 76 which is recombinantly produced.
93. The isolated polypeptide comprising Seq. ID No. 2, 4, 6, 8,10, 12, 16, 18, 20,22, or 24.
- 20 94. A isolated nucleic acid encoding the polypeptide of Claim 76.
95. The polypeptide of claim 39 wherein the protease inhibitor protein comprises Seq ID No. 16,18,20,22, or 24.

1/1

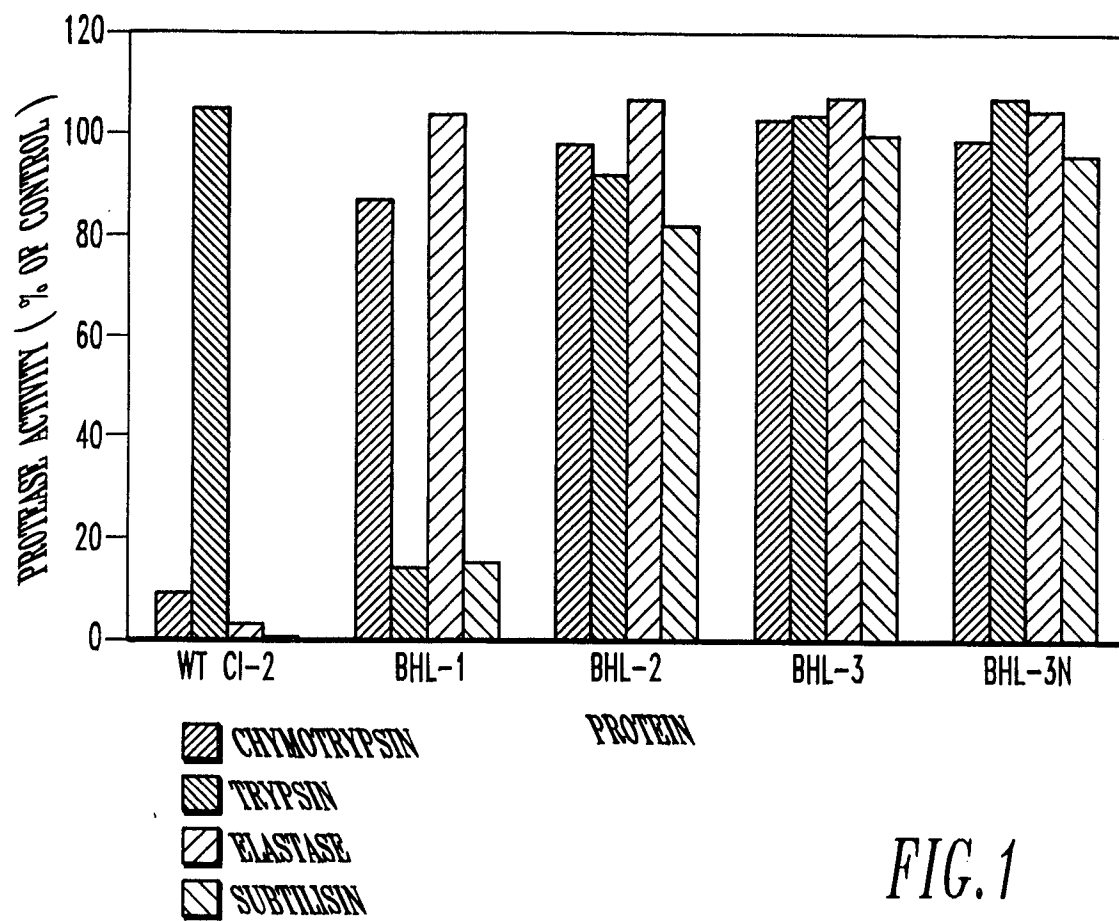


FIG. 1